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Scientific and Technical Information Center

SEARCH REQUEST FORM

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 10-14-05
Art Unit: 1635 Phone Number: 2-0765 Serial Number: 09/486, 757
Location (Bldg/Room#): 2028 (Mailbox #): 2C18 Results Format Preferred (circle): PAPER DISK

To ensure an efficient and quality search, please attach a copy of the cover sheet, claims, and abstract or fill out the following:

Title of Invention: Gytochrome P-450 redox
Inventors (please provide full names): KUTCHAN et al.

Earliest Priority Date: 7-3-00

Search Topic:

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known.

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 10

No size limits NA 2649
may

Please Include interference
Search.

Thanks

10/20/05
JH

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OCT 14 2005

TECH/CHEM. DIVISION
(STIC)

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 19, 2005, 07:23:55 ; Search time 11004 Seconds
(without alignments)
11664.655 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcagctttagtat.....tttgagaaaaa 2649

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2645.8	99.9	2650	8	PSU67185
2	1126.4	42.5	2498	8	AF302496 Hybrid po
3	1104.8	41.7	2617	8	VIRNADPH4
4	1094.8	41.3	2641	8	VSNER
5	1086.2	41.0	2633	8	AY170374
6	1071.6	40.5	2693	8	AB086169
7	1061.4	40.1	2685	8	BT013756
8	1039	39.2	2079	8	AY596976
9	1030.8	38.9	2059	8	AY520902
10	997.2	37.6	2340	8	AY054688
11	994.6	37.5	2079	8	BT008426
12	987.6	37.3	2199	8	ATATRL1G
13	985	37.2	2114	6	A75959
14	969.8	36.6	2561	8	ECU67186
15	918.6	34.7	2493	8	AF302497
16	912.6	34.5	2631	8	PM44CPR
17	911.2	34.4	2610	8	AF302498
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19	895.4	33.8	2136	6	AX651759

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25	873.6	33.0	2618	8	CRCPR
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ALIGNMENTS

RESULT 1	PSU67185	2650 bp	mRNA	linear	PLN 06-MAR-1998
LOCUS	Papaver somniferum NADPH:ferrihemoprotein oxidoreductase mRNA,				
DEFINITION	complete cds.				
ACCESSION	U67185				
VERSION	U67185.1	GI:2580496			
KEYWORDS	Papaver somniferum (opium poppy)				
SOURCE	Papaver somniferum				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales; Papaveraceae; Papaver.				
REFERENCE	1 (bases 1 to 2650)				
AUTHORS	Rosco,A., Pauli,H.H., Priesner,W. and Kutchan,T.M.				
TITLE	Cloning and heterologous expression of NADPH-cytochrome P450 reductases from the Papaveraceae				
JOURNAL	Arch. Biochem. Biophys. 348 (2), 369-377 (1997)				
MEDLINE	98096363				
PUBMED	9434750				
REFERENCE	2 (bases 1 to 2650)				
AUTHORS	Rosco,A. and Kutchan,T.M.				
TITLE	Direct Submission				
JOURNAL	Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie, Universitaet Muenchen, Karlstrasse 29, Munich 80333, Germany				
FEATURES	Location/Qualifiers				
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W"

ORIGIN

Query Match		99.9%;	Score 2645.8;	DB 8;	Length 2650;	
Best Local		99.9%;	Pred. No. 0;			
Matches 2647;		Conservative	0;	Mismatches	2;	Indels 0; Gaps 0;
Qy	1	CGGCACGAGCTTGTAGTATCTTCTAGGGTTTCAAAAGACACAGGAGAGCAAAAGT	60			
Db	1	CGGCACGAGCTTGTAGTATCTTCTAGGGTTTCAAAAGACACAGGAGAGCAAAAGT	60			
Qy	61	CGAATCTTACCTGAAATACATTCGATTGCTTCTCTCTGTTTAAAGCTTCAGAGTCTCTGCTA	120			
Db	61	CGAATCTTACCTGAAATACATTCGATTGCTTCTCTCTGTTTAAAGCTTCAGAGTCTCTGCTA	120			
Qy	121	ATTATGGGTTTCAATTAATTTAGCTAATTCGATTGAAATCGATGTTAGGAATATCAATAGGA	180			
Db	121	ATTATGGGTTTCAATTAATTTAGCTAATTCGATTGAAATCGATGTTAGGAATATCAATAGGA	180			
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Db	301	TATAAACCAATATTTGATAAAGAGAGAGGAGATTGAATTCCTGGTAAATTAAG	360			
Qy	361	CTCAGTATATTTTGGTACTCAGACTGGTACTGCTGAAGATTTCGTAAGGCATTGGCA	420			
Db	361	CTCAGTATATTTTGGTACTCAGACTGGTACTGCTGAAGATTTCGTAAGGCATTGGCA	420			
Qy	421	GAAGAAATTAAGGCAAGTACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTAT	480			
Db	421	GAAGAAATTAAGGCAAGTACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTAT	480			
Qy	481	GCAGCCGAGGATGATCAATATGAAGAGAAATTAAGAAAGAGTCTTTTGGTATTCATG	540			
Db	481	GCAGCCGAGGATGATCAATATGAAGAGAAATTAAGAAAGAGTCTTTTGGTATTCATG	540			
Qy	541	GTAGCCACTTATGGTGTGTGAGCCCACTGACAACTGCTCGAGATTTTACAAATGGTTC	600			
Db	541	GTAGCCACTTATGGTGTGTGAGCCCACTGACAACTGCTCGAGATTTTACAAATGGTTC	600			
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Db	841	GAGGATGCTGCTCTTCACTGGCTACACCGTATATTTGCTACTGTTCTCGAATACAGGGTA	900			
Qy	901	GTGATTTCAGAAACTACGGTCCGGCTCGGATGATAAACAATAAATACTGCTAACCGC	960			
Db	901	GTGATTTCAGAAACTACGGTCCGGCTCGGATGATAAACAATAAATACTGCTAACCGC	960			
Qy	961	GATGTTGCAATTTGATATTTCCATCTTTCAGAACCAATTTGTTGCTCAACAAAGAGAGCTC	1020			
Db	961	GATGTTGCAATTTGATATTTCCATCTTTCAGAACCAATTTGTTGCTCAACAAAGAGAGCTC	1020			
Qy	1021	CACAAACCAAGTCTGATAGATCTGTATATCATCTGGAGTTTCAGATATCAGGCTCTTCC	1080			
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Qy	1081	CTTTACATATGAGACTGGAGATCATGTTGTTTATGCTGAGAACTGCGATGAAACTGTC	1140			
Db	1081	CTTTACATATGAGACTGGAGATCATGTTGTTTATGCTGAGAACTGCGATGAAACTGTC	1140			
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Db	1201	AAAGAAGCAGGCTCACCCAGGGAAGCTCATTTACACCTCTTCCAGGTCCTTGCACC	1260			
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Db	1261	TTACGATCTGCTCCTAGCAGCTATGCTGATCTTTTGAATCTCTTGAAGAGGCTCTCTCG	1320			
Qy	1321	ATTGCTCTGCTCCGCTCATGCACTCTGTAACCCAGTGAAGCAGAGAGATGCGCTTTTGTCA	1380			
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Db	1561	AGAAATCATGTCGCTGCTTTAGTATATGTTCAAGCCCTTACCGAAGGTTTCAACCGA	1620			
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Db	1621	GGAGTGTGTTTCCACATGAGTGAAGCATGCAAGTTTCTCAGGATAGCTGGGCTCTATTTT	1680			
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Db	1681	GTTTCGAAAGTCAAACTTCAAGTTTACCGCTGACCCCTCAACTTATCATGTTGTTGGA	1740			
Qy	1741	CTTGGTACAGGGTTAGCTCTTTCAGAGGATTTCTGACGAAAGATGSCCTCAAGGAA	1800			
Db	1741	CTTGGTACAGGGTTAGCTCTTTCAGAGGATTTCTGACGAAAGATGSCCTCAAGGAA	1800			
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Qy	2221	TGGTTTCTATTATATTATTTGATCTCCTCTCGAAAATCCCAAGCACTTCCAGACATCCCTC	2280
Db	2221	TGGTTTCTATTATATTATTTGATCTCCTCTCGAAAATCCCAAGCACTTCCAGACATCCCTC	2280
Qy	2281	GATTCTTCTCCAGTGGTTCCAAATCGAAGCTCGTATAAATGAGAGCAGTGCAAATTGTG	2340
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Qy	2581	TTCTTGTGTTTCTTATGGCTACCGAGAGGAGCTATATAATGTCATTTAGAGTTTGGAGAAA	2640
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Db	2641	AAAAAAAAAAAA 2649	

RESULT 2	AF302496	2498 bp	linear	PLN 13-DEC-2002
LOCUS	AF302496			
DEFINITION	Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome P450 oxydoreductase isoform 1 mRNA, complete cds.			
ACCESSION	AF302496			
VERSION	AF302496.1	GI:13183561		
KEYWORDS	.			
SOURCE	Populus balsamifera subsp. trichocarpa x Populus deltoides			
ORGANISM	Populus balsamifera subsp. trichocarpa x Populus deltoides			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids 1; Malpighiales; Salicaceae; Saliceae; Populus.			
REFERENCE	1 (bases 1 to 2498)			
AUTHORS	Ro, D.K., Ehrling, J. and Douglas, C.J.			
TITLE	Cloning, Functional Expression, and Subcellular Localization of Multiple NADPH-Cytochrome P450 Reductases from Hybrid Poplar			
JOURNAL	Plant Physiol. 130 (4), 1837-1851 (2002)			
PUBMED	12481067			
REFERENCE	2 (bases 1 to 2498)			

Ro,D.-K. and Douglas,C.
 Direct Submission
 Submitted (05-SEP-2000) Botany, University of British Columbia,
 6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada
 Location/Qualifiers
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 source

[illegible]

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Db 1628 TCTGGAGAAAAGTTATGAATGATGTGGGCTCCCATTTTTTCCACAGAACATCTAATTTCAA 1687
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Db 1928 GCCACAGAAGGAATATGTTTCAACATAAGATGCTGGATAGACGACGAGATATGGACTAT 1987
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RESULT 3
VIRNADPH4
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
FEATURES
source

VIRNADPH4 2617 bp mRNA linear PLN 23-APR-2001
Vigna radiata NADPH cytochrome P450 mRNA, complete cds.
L07843
L07843.1 GI:295447

Vigna radiata
Vigna radiata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Vigna.
1 (bases 1 to 2617)
Shet,M.S., Sachasivan,K., Arlotto,M.A., Mehdy,M.C. and
Estabrook,R.W.
NADPH-cytochrome P450 reductase from mung bean
Proc. Natl. Acad. Sci. U.S.A. 90 (7), 2890-2894 (1993)
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Query Match 41.7%; Score 1104.8; DB 8; Length 2617;
Best Local Similarity 75.4%; Pred. No. 3.2e-249;
Matches 1421; Conservative 0; Mismatches 442; Indels 21; Gaps 3;

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Qy	371	TTTTTGTACTCAGACTGTTACTGCTCAAGGATTTGCTAAGGATTTGGCGAAGAAATTA	430
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Db	488	AGCAAGGTATGAAAAGCGCGTGTCAAGTTGTGACCTGGATGACTATGCAGCTGATG	547
Qy	491	ATGATCAATATGAAGAGAAATTAAGAAAGAGTCTTTGGTGTGTTTTCATGCTAGCCACTT	550
Db	548	ATGATCTATATGAGGAGAGCTGAAGAAAGAGTCTTTGATTTTTCATGCTAGCAACTT	607
Qy	551	ATGCTGATGTGAGCCAACTGACAAATGCTCGAGATTTTACAAATGGTTCACTCAG--	607
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Qy	608	AACATGAAGGGGAGAGTGGCTTCAGCAACTTAATCTATGTTGTTTGGTTGGGTAAACC	667
Db	668	AAGACGAAAGGGAATCTGCTCTCAAAACTCACTATGAGGTTTTCGGCTAGGTAAACA	727
Qy	668	GTCATACGAGCACTTTCAACAAGATCGCGTAGATGAGCAACTCGGTAAACAAG	727
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Qy	728	GTCAAAAGCCGATTTTCAAGTGGGCTCGGTGACGATGATCAATGATGAAGATGATT	787
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Qy	788	TTACTCTTGGCGAGATTTGCTGGACTGCAATTTGGATCAGTTGCTCAAGATGAGGATG	847
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Qy	908	ACGAAACTACGGTGGGCTCTGGATGATTAACACATATAACTGCTTAAGCGCGATGTTG	967
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Qy	1028	CCAAGTCTGATAGATCTGTPATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACAT	1087
Db	1088	CTGAGTCTGATCTGTTCTTGATACATTTTGGAAATTTGATATATCGGGAGCAGCATTAACAT	1147
Qy	1088	ATCAGACTGGAGATCATTTGTTGTTTATGCTGAGAACTCGCATGAAACTGTGCGGGAAG	1147
Db	1148	ATGATACTGAGACCAATGTGGTGTGTTATGCTGAGAACTGCAATGAATCTGCGAAGAA	1207
Qy	1148	CAGGGAAGCTTTGGGTCAACCCCTGGATTTGCTGTTTCAATTCACAGGATAAAGAG	1207
Db	1208	CTGGGAAGTTGTTGGGTCAAGATTTGGATCTATTTTTTCTCTTACACAGACAAGGATG	1267
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RESULT 4
VSFNR
LOCUS
DEFINITION
ACCESSION

V. sativa mRNA for NADPH-ferrihemoprotein reductase.
2641 bp mRNA linear PLN 14-SEP-1993
Z26252


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QY 908 ACGAAACTACGGTCCGGCTCTCGGATGATATAACACATAAATACCTGCTAACCGCGGATGTTG 967
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Db 2141 GTGATGCTNAGGCGATGGCCGAGATGTTTCATCGGACTCTTTCATACCATTTGCCAGCAGC 2200
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Db 2261 GTTATCTTAGAGATGTCTGGTAA 2283

RESULT 6
AB086169
LOCUS
DEFINITION
AB086169 2693 bp mRNA for NADPH-cytochrome P-450 reductase,
complete cds.
ACCESSION
AB086169
VERSION
AB086169.1 GI:26106070
KEYWORDS
Ophiorthiza pumila
SOURCE
Ophiorthiza pumila
ORGANISM
Ophiorthiza pumila
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Gentianales; Rubiaceae; Rubioideae;
Ophiorthizeae; Ophiorthiza.
REFERENCE
1 Yamazaki, Y., Sudo, H., Yamazaki, M., Aimi, N. and Saito, K.
Camptothecin Biosynthetic Genes in Hairy Roots of Ophiorthiza
pumila: Cloning, Characterization and Differential Expression in
Tissues and by Stress Compounds
Plant Cell Physiol. 44 (4), 395-403 (2003)
JOURNAL
MEDLINE
22608538
PUBMED
12721380
REFERENCE
2 (bases 1 to 2693)
Yamazaki, Y., Yamazaki, M. and Saito, K.
Direct Submission
Submitted (04-JUN-2002) Mami Yamazaki, Graduate School of
Pharmaceutical Sciences, Chiba University, Department of Molecular
Biology and Biotechnology; 1-33 Yayoi-cho, Inage-ku, Chiba-shi,
Chiba 263-8544, Japan (E-mail:mamiy@p.chiba-u.ac.jp,
Tel:81-43-290-2906, Fax:81-43-290-2905)
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1. (bases 1 to 2685)	
Kirkness,E.P., Wang, W. and Vazeille, A.	
Direct Submission	
Submitted (11-MAY-2004) The Institute for Genomic Research, 9712	
Medical Center Drive, Rockville, MD 20850, USA	
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QY	520 GTTTTGCCAAAGCTTTATCAGAGGAGATAAAGCAAGATATGAGAAGGCAGTTGTGAAG 579
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QY	581 CGAGATTTTACAAATGGTTCACCTCAGGAACATGAAAGGGGAGAGTGGCTTCAGCAACTAA 640
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QY	1000 CAATTCCTGAAATATCGTTTGGTTTATCCATGATACCACTAT---GAGTCTTGGAGATAAGC 1056
DB	941 ACATAAATACTGCTAACCGCGATGTTGCAATTTTGATATTTCTCCATCTTTCAGAACCAATTG 1000
QY	1057 ATCGAGCATGGCTAATGGGAATACCAATATGATATCCACCACTGCAAGTCAATG 1116
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QY	1117 TGGCTGTTCAGAGAGAGCTTTCACACCCCGAGTCTGATCGCTCATGTATACATCTGGAGT 1176
DB	1061 TCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATGTGTTGGTGTATTGCTG 1120

DB	1177 TTGATATATCTGGCACTGGGATTTCTATGAAACAGGAGATCATGTGGGTGTTATGCTG 1236
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DB	1241 CTTTCCCAAGTCTCTTGACCTTACGATCTGCCTTAGCACGCTATGCTGATCTTTTGAATC 1300
QY	1297 TATTCCTATTATACCCGACAAAGGAGATGGTACAGCTGGAGGAGGCTCGTTACCCCCAC 1356
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DB	1946 AGAAGGAATATGTTTCAACATAAGATGATGGAGAAAGCAACGGATGTATGGAATGTGATAT 2005
QY	2077 AGAAGAGTATGTTTCAACACAAATGATGGAAGAAAGCTTCCCATGTTTTCGAGTTTAATCT 2136
DB	2006 CAGGGGACGGTTATCTCTATGTGTGGTGTGTCGCAAGGAAATGGCCAGAGATGTCATC 2065
QY	2137 CTCAGGAGGATATCTATATGTATGTGGGGATGCTAAAGGGATGGCCAGAGACGTACATC 2196
DB	2066 GCAGGTTGCATACCAATTCGCCCAAGAACAGGACCCCATGGAATCATCTGCTGCCGAAGCTG 2125
QY	2197 GTACACTCCATACCATAGTCCAGGACGAGAGATCGCGACTCATCCAAAGCAGAGGCTG 2256
DB	2126 CAGTAAAGAAACTCCAAAGTTGAAGACGATATCTTAAGAGATGTCTCGTGAT 2176

Db 2257 TTGTAAAGAACTCCAAATGGATGGAAGATATCTCAGGGATGTGTGGTAAT 2307

RESULT 8
AY596976
LOCUS
DEFINITION
Centaurium erythraea NADPH:cytochrome P450-reductase mRNA, complete cds.
ACCESSION
AY596976.1 GI:46403206
VERSION
AY596976.1
KEYWORDS
Centaurium erythraea
SOURCE
Centaurium erythraea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; asterids; lamiids; Gentianales; Gentianaceae; Centaurium.
REFERENCE
1 (bases 1 to 2079)
Schwarz, H. and Beerhues, L.
Molecular cloning of NADPH:cytochrome P450-reductase from Centaurium erythraea cell cultures
Unpublished
2 (bases 1 to 2079)
Schwarz, H. and Beerhues, L.
Direct Submission
Submitted (08-APR-2004) Institut fuer Pharmazeutische Biologie, Universitaet Braunschweig, Mendelssohnstrasse 1, Braunschweig 38106, Germany
FEATURES
Location/Qualifiers
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MNGRYLRDVM"

ORIGIN

Query Match 39.2%; Score 1039; DB 8; Length 2079;
Best Local Similarity 72.7%; Pred. No. 1e-233;
Matches 1361; Conservative 0; Mismatches 495; Indels 15; Gaps 1;
QY 320 AAGAAGAGGAGGATGAAGTTGATCCCTGGTAAATTAAGCTCACTATATTTTGGTA 379
DB 209 AGGAGGAGGAGGAGGAGTTGGATCCCTAGCAAGTTAAGGTACCGTGTGTGGTA 268
QY 380 CTGAGACTGTCTGCTGAAGGATTTGCTAAGGCATTGGCAGAGAAATTAAGCAAGT 439
DB 269 CACAGACTGGACTGCTGAGGTTTGTCTAAGGCATTGGCAGAGAGATCAAGCAAGT 328
QY 440 ACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACGCCGAGGATGATCAAT 499
DB 329 ATGAGAAAGCAGTTGTTAAAGTAGTTGATTTGGATGATTATGCTGCTGATGATGACCAAT 388
QY 500 ATGAGAGAAATTAAGAAAGAGCTCTTTGGTGTGTTTTTCATGTTAGGCCACTATGTTGGTATG 559
DB 389 ATGAGGAAATTAAGAAAGAGACCTTGGCATTTTTCATGTTGGTGGCCACTATGTTGGTATG 448

QY 560 GTGAGCAACTGACAACTGCTGCAGATTTTTTACAAATGGTTTCACTCAGGAACATGAAGGG 619
DB 449 GAGAGCAACTGATAATGCTGCTCGGTTTTTACAAATGGTTTTTCGAGGTTAAAGAAAGGG 508
QY 620 GAGAGTGGCTTCAGCAACTAATTTATGGTGTGTTTTTGGTGGTAAACCGTCAATACGAGC 679
DB 509 AGCCCTGGCTTCAGCAACTTACATATGGGGTTTTTGGTGGTAAACCGTCAATATGAAC 568
QY 680 ATTTCAACAGATCGCGGTAGATGTGGATGAGCAACTCGGTAAACAGGTGCAAGCGCA 739
DB 569 ATTTCAATAGATTGGGAAGGTGATCGATGACCAACTTATTTGAACAGGTGCAAGGAAGA 628
QY 740 TTCTTCAAGTGGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTTACTGCTGGC 799
DB 629 TTGTACCACTTGTCTTGGTGATGATGACCAATGATTTAGGATGATTTTCTGCTTGA 688
QY 800 GAGAAATTTGTGGATGCAATTTGGATGATGCTCAAGATGAGGATGCTGCTCTTCAG 859
DB 689 GAGATCAACTTTGGCCAGAACTTGTATAAATCTTTTGGATGAGGATAGTTCACTGCTG 748
QY 860 TGGCTACACCGTATATTTGCTACTGTTCTGCAATACAGGGTAGTGATTCAGAAACTACGG 919
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QY 920 TCGCGCTCTGGATGATAAACAATATACTGCTAACGCCGATGTTGCAATTTGATATTC 979
DB 809 CTGATTTCTATGAAATAGCAATTGCAATGATGATGATGATGATGATGATGATGATGAT 868
QY 980 TCATCTTTGCAGAACCAATTTGTTGCTCAACAAAGAGAGCTCCACAAACCCAGCTGTGATA 1039
DB 869 AACACCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 928
QY 1040 GATCTGTATACATCTGGAGATTCGACATATCAGGCTCTTCCCTTATATATGACACTGGAG 1099
DB 929 GCTCATGCTATTTGGAATTTGATATAGCTGGCAAGGATTAATATGAAACTGGAG 988
QY 1100 ATCATGCTGGTGTATATGCTGAGAACTGCGATGAAACTGTCGAGGAGGAGGAGGAGCTGT 1159
DB 989 ATCAGTGGGTGTATGCTGAGAAATTTGAGAGAAATTTGAGAGAGCTGCAAGATTGT 1048
QY 1160 TGGGTCAACCCCTGGATTTGCTGTTTCAATTCACAGGATAAAGAGAGCGGTCAACCC 1219
DB 1049 TGGGTCAATCTTTAGACTTGAATTTTCAATCCTGCTGCAAGAGGATGGCACACCT 1108
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DB 1109 TGGGAGGCTCATTTGGCTCTCTCTTCCAGGGCTTTCACCTTTCGAACTGCACTTGTCT 1168
QY 1280 GCTATGCTGATCTTTTGAATCTCTTAGAAAGGCTTCTCTGATTTGCTCTGCTGCTCATG 1339
DB 1169 GTTATGCTGATCTTAACTCTCTCCCAAAAGACAGCTTTGATTTGCTTTAGCTGCTCAT 1228
QY 1340 CATCTGTACCCAGTGAAGCAGAGATTCGGCTTTTGTTCATCCTCTGCGGAAAGATG 1399
DB 1229 CAAGTGAACCAAGCGAAGCAGAAAGGCTAAATTTCTTATCATCTCAGCAGGGAAGGATG 1288
QY 1400 AGTATTTCAAAATGGGTAGTTGGAGCTCAGAGGATCTTTTGGAGATCATGGCCGAGTTTC 1459
DB 1289 ATTATTTCAAAATGGATCGTGGGAAGTCAGAGAAGTCTCTTGAAGTTATGGGCTGAATTC 1348
QY 1460 CATCAGAAAACCCCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1519
DB 1349 CTTTCAGAAAACCTCTCTTGGGATATTTTTCAGCTATAGCACCTCAATATACAGCCCC 1408
QY 1520 GATATCTATCTATCTCATCT 1579
DB 1409 GTTACTACTCTATCT 1468
QY 1580 CTTTAGTATATGTTCAAGCCCTTACCGGAAGGGTTTCCAGCAGGAGTGTGTTTCGACATGGA 1639
DB 1469 CGCTAGTTTATGGGCTTACTCTCTACAGGGCGTATTTACAGAGAGAGTGTGTTTCAACTTGA 1528
QY 1640 TGAAGCATGCAGTTCC-----TCAGGATAGCTGGGCTCCTATTTTGTTC 1684

Db	1529	TGAGAAATGCGATTCCATCAGAAAGGAGCCATGATCTAGCCAGGCGCTGTTTTATCA	1588		
QY	1685	GAACGTCAAATCTCAAGTTACACGCTGACCCCTCAACTCCAATATCATGGTGGGACCTG	1744		
Db	1589	GGACATCAAATTTCAAATACACAGCTGATCCTTCCATTCCTCAATGTTATGATAGGACCTG	1648		
QY	1745	GTACAGGTTAGTCTCTTTTCAGAGGATTTCTGAGGAAGAATGGCCCTCAAGGAAATG	1804		
Db	1649	GAACCGGTCTGGCTCCATTTAGAGGATCTTACAGGAAAGATTTGTCTGAAGGAAGAAG	1708		
QY	1805	GTGCTCAACTTGCGCCAGCAGTCTCTTTTTCGGATGTAGGAATCGTAATATGGACTTCA	1864		
Db	1709	GTGCTCAACTTGGTCTGCTCTATTGTTCTTTGGTTGAGAAATCGCAGATGGATTCCA	1768		
QY	1865	TTTATGAAGACGAACTAAACAACCTTCGTGGAAAGAGGAGTCATTTTCGGAGCTAGTTATTG	1924		
Db	1769	TTTATGAGAGCGAGTTGAAAAAATATGAGGATGAAGGTGTAGTATCCGAGTTGATAGTTG	1828		
QY	1925	CTTTTTCAGTGAAGGGGAAAGAGGAATATGTTCAACATAAGATGATGGAGAAAGCAA	1984		
Db	1829	CATTTTCAAGGGAGGGGCCACAGAGGAATATGTGCAACATAAGATGATGGAAGGCAG	1888		
QY	1985	CGGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGTGATGCCAAGG	2044		
Db	1889	CCGAATCTGGAGTTTGCTCTCCAGAGGGGTATCTTTACGTATGTGGAGATGCTAAGG	1948		
QY	2045	GAATGCCAGAGATGTCATTCGCACCGTTGCATACCATTCGCCAAGAACAGGGACCCATGG	2104		
Db	1949	GTATGGCAAGAGACGTTTCATCGTGTCTCTTCATACCATTTGTTCAAGAGCAGGAAAGACGG	2008		
QY	2105	AATCATCTGTCGCGAAGCTGCAGTAAAGAAACTCCAAAGTTGAAGAACGATATCTAAGAG	2164		
Db	2009	ATTCTTCAAGGGCGGAGGCTATCGTGAACAGCTACAGATGAATGGGCGGTATCTAAGG	2068		
QY	2165	ATGCTCTGGTGA	2175		
Db	2069	ATGTTTGGTGA	2079		
RESULT 9	AY520902	2059 bp	mRNA	linear	PLN 01-FEB-2004
LOCUS	Hypericum androsaemum NADPH:cytochrome P450-reductase mRNA,				
DEFINITION	complete cds.				
ACCESSION	AY520902				
VERSION	AY520902.1	GI:41350272			
KEYWORDS					
SOURCE	Hypericum androsaemum				
ORGANISM	Hypericum androsaemum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Clusiaceae; Hypericum.				
AUTHORS	1 (bases 1 to 2059)				
TITLE	Schwarz,H. and Beerhues,L.				
JOURNAL	Molecular cloning of NADPH:cytochrome P450-reductase from Hypericum androsaemum cell cultures				
REFERENCE	Unpublished				
AUTHORS	2 (bases 1 to 2059)				
TITLE	Schwarz,H. and Beerhues,L.				
JOURNAL	Submitted (08-JAN-2004) Institut fuer Pharmazeutische Biologie, Universitaet Braunschweig, Mendelssohnstrasse 1, Braunschweig 38106, Germany				
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		GPALLPFGCRNRQMDYIYEEELNFFVEQALSSELIVASREPGFDKYVQHKMDKAAAY	
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		NWV"	
ORIGIN			
	Query Match	38.9%;	Score 1030.8; DB 8; Length 2059;
	Best Local Similarity	72.4%;	Pred. No. 8.8e-232;
	Matches 1357;	Conservative 0;	Mismatches 502; Indels 15; Gaps 1;
QY	318	TAAAGAAGAAGAGGAGATTGAAGTTGATCCTCGTAAAAATTAAGCTCACATATATTTTTTGG	377
Db	186	TAAGGAGGAGGAGGAGAGACGAGCCCGAGGGAGACCAAGGTCGCACTCTTCTACGG	245
QY	378	TACTCAGACTGTACTGCTGAAGGATTTGCTTAAGGCATTTGGCAGAGAAGAAATTAAGCAAA	437
Db	246	CACCCAGACCGGCACCTGCCGAGGGATTCGCCAAGGCTTTGGCTGAGGAGATCAAGGTTGC	305
QY	438	GTACAAGAAGACAGTTGTTAAAGTAGTTCACCTGGATGACTATGCAGCCGAGGATGATCA	497
Db	306	ATATGAAAAGCAGTGTCTCAAAAGTTGTTGACTTGGATGATTAATGCTTTCGATGATGATCA	365
QY	498	ATATGAAGAAGAAATTAAGAAGAGTCTTTTGGTGTGTTTTTTCATGGTAGGCACCTTATGGTGA	557
Db	366	ATATGAAGAAGAGCTGAAAAAGGAGACCTTTGGCTTTTTCATGGTGGCCACGATATGGGA	425
QY	558	TGGTAGGCCAACTGACAAATGCTCGGAGATTTTACAAATGGTTTCACTCAGAACATCAAG	617
Db	426	TGGAGAACCTACTGATGAACGAGCCCGATTTTACAAAGTGTGTTTCACTGAGGAACATCAAG	485
QY	618	GGGAGAGTGGCTTCAGCAACTAACTTATGGTGTGTTTTGGTGTGTTGGGTAAACCGTCAATACGA	677
Db	486	GGGAGTCTGGCTTCAACAACTCAAAATTTGGTGTATTCGGTCTTTGGTAATCGCCAAATATGA	545
QY	678	GCATTTCAAAGAATCGCGGTAGATGTGGATCAGCAACTCGGTAAACAAGGTGCAAAAGCG	737
Db	546	ACATTTCAAAGAATAGCTAAGGTGCTTGATGAACAAATCTCTGTGAACAAGGAGCTAAGCG	605
QY	738	CATTGTTCAAGTGGGGCTGGTGACGATGATCAATGCAATTGAAGATGATTACTGCTTG	797
Db	606	CCTCATTCCTGTGGGCTCGGTGATGATCAGTGCATTTGAGGATGATTTTCACTGCTTG	665
QY	798	GGGAGAAATGTTGTGACCTGAATTTGATCAGTTGCTCAAGATGAGGATGCTGCTCTTC	857
Db	666	GAGAGAAATTTATGGCTTGAGCTGATCCATTTGCTAAGAGATGAAGATATGCGAATGC	725
QY	858	AGTGGCTACACCGTATATTGCTTACTGTTCTCTGAATACAGGGTAGTGATTTACGAAACTAC	917
Db	726	TGCATCTACACCATACACTGCAGCTATATACTTGAATATCGTGTGTTTATTTCATGATCAAC	785
QY	918	GGTGGGGCTCTGGATGATAAACAATAACTGCTTAACGGGATGTTTGCATTTCATAT	977
Db	786	GACGCTATCAGTCGAGGATTAAGTTTTCGAAATTTGGCGAAACGGGAATGCAACTTTTATGC	845
QY	978	TCTCCATCTTCGAGAAACCATTTGTTGCTCAACAAAGAGAGCTCCCAAAACCCCAAGTCTGA	1037
Db	846	TCAACATCCATCGAGGGTTAATGTTGCTGTCCAGAGAGAGCTTCACAAGCCGAGTCTGA	905
QY	1038	TAGATCTCTATATCATCTGGAGTTGACATATACAGGCTTCTCCCTTACATATGAGACTGG	1097
Db	906	CCGGTCATGCATACATCTGGAATTTGACATATCAGGACTGTTTATTTAGATACGAAGCTGG	965

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ORIGIN		Query Match		Best Local Similarity		Matches 1349; Conservative		Score 997.2; DB 8; Length 2340;		Pred. No. 7.2e-224; Indels 18; Gaps 2;		Mismatches 523; Indels 18; Gaps 2;	
Qy	310	ATAATTGAT	AAGAAGAGGAGATTGAAGTTGATCTCGTGGTAAAAATTAAGCTCACTATA	369.									
Db	291	ATGCTAAGG	ACGAGGATGATGATTGGATTTGGGATCCGGGAAGACTAGAGTCTCTATC	350									
Qy	370	TTTTTTGGT	ACTCAGACTGCTAGCTGAGGATTTGCTTAAGGCATTGGCAGAGAATTT	429									
Db	351	TTCTTCGGT	ACGAGACTGGAACAGCTGAGGGATTTGCTAAGGCATTTATCCGAAGAAATC	410									
Qy	430	AAGCAAAAG	TACAAGAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACGCCGAG	489									
Db	411	AAAGCGGAT	ATGAAGAAGCAGCAGTCAAGTCAATTGACTTGGATGACTATGCTGCCGAT	470									
Qy	490	GATGATCAAT	ATGAAGAAAATTAAGAAAAGAGCTTTTGGTGTGTTTTCATGTTAGGCCACT	549									
Db	471	GATGACAGT	ATGAAGAAAATTAAGAAAAGAACTTTGGCAATTTTCTGTGTTGCTACT	530									
Qy	550	TATGGTGAT	GGTGCCCACTGACAACTGCTGCGAGATTTTACAATGCTTCACTCAGGAA	609									
Db	531	TATGGAGAT	GGAGGCGCTACTGACAACTGCTGCCAGATTTTACAATGCTTACGGAGGAA	590									
Qy	610	CATGAAGCG	GAGAGTGGCTTCAGCAACTAACTTATGGTGTGTTTGGTGGGTAAACCGT	669									
Db	591	AATGACGGG	ATATAAGCTTCAACACTAGCATATGGTGTGTTTGGTCTTGGTAAATCGC	650									
Qy	670	CAATACGAG	CAATTAACAGATCGCGGTAGATGTGGATGAGCAACTCGGTAAACAAGGT	729									
Db	651	CAATATGAA	CAATTAATAAGATCGGATAGTCTTGGATGAAGAGTTATGTAAGAAAAGGT	710									
Qy	730	GCAAGCGCA	TGTTTCAAGTGGGCTCGGTGACGATGATCAATGCAATTGAAGATGATTTT	789									
Db	711	GCAAGCGCT	TTATTAAGTTCGCTAGGAGATGATGATCAGAGCAATTGAGGATGATTTT	770									
Qy	790	ACTGCTTGG	CGAGAAATTTGTTGGACTGAAATGGATGGATCGTCAAGAGATGAGGATGCT	849									
Db	771	AATGCGCTG	GGAAGAAATCACTATGCTGAGCTAGACAAAGCTCTCAAGACGAGGATGAT	830									
Qy	850	GCTCCTTCA	GCTGACACCGTATATTTGCTATGTTCTCGTGAATPACAGGGTAGTATCAC	909									
Db	831	AAAAAGT---	GTGGCAACTCTTATACAGCTGTTTATTCCTGAAATACCGGGTGGTGACTCAT	887									
Qy	910	GAAACTACG	TCGGGCTCTGGATGATAACACATAAATACTGCTAACCGCGATGTGCA	969									
Db	888	GATCCTCGG	TTTACAATCAAAATCAATGGAATCAAAATGTGCCAATGGAATACTACT	947									
Qy	970	TTTGTATAT	TCCTCCTGACAGAACCATTTGTTGCTCAACAAAGAGAGCTCCCAAAACCC	1029									
Db	948	ATTGACATTC	ATCATCCCTGACAGTTGATGTTGCTGTCGAGAGGAGCTTTCACACAT	1007									
Qy	1030	AAGTCTGAT	AGATCTGATATATCTAGGATTCGACATATCAGGCTCTTCCCTTACATAT	1089									
Db	1008	GAATCTGAT	CGGCTTGGATTCATCTCGAGTTCGACATATCCAGGACGGGTATTTACATAT	1067									
Qy	1090	GAGACTGGG	ATGTTGGTGTATGCTGAGAACTGCGCATGAACTGTCGAGGAGCA	1149									
Db	1068	GAAACAGGT	ACCATGTAGGTGATATGCTGAAATCATGTTGAAATAGTTGGAAGAAGCT	1127									
Qy	1150	GGGAAGCTG	TGGGTCAACCCCTGGATTTGCTGTTTCAATTCACACGGATAAAGAAGAC	1209									
Db	1128	GGAAATATG	CTGGCCACTCTTTAGATTTAGTATTTTCCATACATGCTGACAGGAGAT	1187									
Qy	1210	GGGTCACCC	CGGGAAGCTCATTTACCACTCTCTTTCCAGGTCCTTGCACCTTACGATCT	1269									
Db	1188	GGCTCCCCA	TTGGAAGCGCAGTGGCGCTCTCTTTCCCTGCTCCATGACACTTGGGACT	1247									
Qy	1270	GCCTTAGCA	CGCTATGCTGATCTTTTGAATCCTCTTAGAAGAGCTTCTCTGATGCTCTG	1329									

Db	1248	GGTTTGGC	AAAGATACGACAGACCTTTTGAACCTCTCGAAAGTCTCGGTTAGTTCCTTG	1307									
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Db	1308	GCGGCTATG	CCACTGAACCAAGTGAAGCCGAGAACTTTAAGCACCTGACATCACCTGAT	1367									
Qy	1390	GGAAGAATG	AGATGATTTCAAATTTGGGTAGTTGGAAAGTCAAGGAGTCTTTTGGAGATCATG	1449									
Db	1368	GGAAGGATG	AGTAGTACTCAATGGATTTGTCAAAGTCAAGAAAGTCTTTTAGAGGTGATG	1427									
Qy	1450	GCGAGTTTC	CAATCAGCAAAACCCCTCTTGTGTGTTCTTCTGCTGCAGTACGCCCTCGC	1509									
Db	1428	GCTGCTTTT	CCATCTGCAAAACCCCACTAGGTGATTTTGTGTCAAATAGTCTCTCGT	1487									
Qy	1510	TTACGCCCT	CGATCTATTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAAATTCAT	1569									
Db	1488	CTACAACTC	GTACTACTCTCATCTCGCAAGATTGGCGCAAGTAGAGTTCAAT	1547									
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Qy	1630	TCGACATGT	GAAGCATGCAGTTCTCTCAGGA-----TAGCTGGGCTCCT	1674									
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Qy	1675	ATTTTTTGT	TCGAACGCTCAAACTTCAAGTTACAGCTGACCCCTCAACTCCAATTAATCATG	1734									
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Qy	1735	GTGGGACCT	GTGTAAGGTTAGCTCTTTCAGAGATTTTCTGAGGAAAGATGGCCCTC	1794									
Db	1728	GTGGGACCT	GTGGCTGGCTGGCACCTTTTAGAGGTTTCTGCAGGAAAGATGGCACTA	1787									
Qy	1795	AAGGAAATG	GTGCTCAACTTCGCCAGCAGTCTCTTTTTCGGATGTAGGAATCGTAAT	1854									
Db	1788	AAAGAAGAT	GGAGAGAACTAGGTTTCATCTTTGCTCTCTTTGGGTGTAGAAATCGACAG	1847									
Qy	1855	ATGGACTTC	ATTATGAAGACGAACTAAACAACTTCGTGGAACGAGGAGTCAATTCGGAG	1914									
Db	1848	ATGGACTTT	ATATACGAGGATGAGCTCAATAATTTTGTGATCAAGCGCGTAATATCTGAG	1907									
Qy	1915	CTAGTTATT	GGCTTTTACGTGAAGGGGAAAGAGGAATATGTTCAACATTAAGATGATG	1974									
Db	1908	CTCATCATG	CGCATTTCTCCGTGAAGGAGCTCAGAAGGAGTATGTTCAACATAAGATGATG	1967									
Qy	1975	GAGAAGCAA	CGGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTTGT	2034									
Db	1968	GAGAAGCAG	CAAGTTTGGGATCTAATAAGGAAAGAGGATATCTCTATGTATCGGTT	2027									
Qy	2035	GATGCCAAG	GGGAATGGCCAGAGATGTCCATCGACAGTTCGCATACCACTGCCCAAGAACAG	2094									
Db	2028	GATGCTAAG	GGGCATGSCGAGGGGACGTCCACCGAACTCTACACACCACTTGTTCAGGAGCAG	2087									
Qy	2095	GGACCCATG	GAATCATCTCTCGTCCGAGCTGAGTAAAGAAACTCCAAGTTGAGAACGA	2154									
Db	2088	GAAAGTGTG	AGTTCTGTCAGAGGAGGCTATAGTTAAGAAAACCTTCAAAACCGAAGGAAGA	2147									
Qy	2155	TATCTAAGA	GAGATGTCTGGTGATCGAATGTA	2184									
Db	2148	TACCTCAGA	GATGTCTGGTGATTGATGATA	2177									

RESULT 11
BT008426
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

BT008426
Arabidopsis thaliana At4g24520 gene, complete cds.
BT008426.1
GI:30725525
FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana

2079 bp
mRNA
linear
PLN 15-MAY-2003

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1. (bases 1 to 2079)
 Cheuk, R., Chen, H., Kim, C.-J., Shinn, P., Bowser, L., Carninci, P., Dale, J. M., Hayashizaki, Y., Hsuan, V. W., Ishida, J., Jones, T., Kariya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C., Wu, H. C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R. W., Theologis, A. and Ecker, J. R.
 Arabidopsis ORF clones
 Unpublished

TITLE
 JOURNAL
 REFERENCE
 AUTHORS

2. (bases 1 to 2079)
 Cheuk, R., Chen, H., Kim, C.-J., Shinn, P., Bowser, L., Carninci, P., Dale, J. M., Hayashizaki, Y., Hsuan, V. W., Ishida, J., Jones, T., Kariya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Toriumi, M., Wong, C., Wu, H. C., Yamada, K., Yu, G., Yuan, S., Shinozaki, K., Davis, R. W., Theologis, A. and Ecker, J. R.
 Direct Submission

TITLE
 JOURNAL

Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory (SIGAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

COMMENT

RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: "RIKEN Arabidopsis Full-length cDNA"): Seki, M., Narusaka, M., Ishida, J., Satou, M., Kamiya, A., Sakurai, T., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.

The Salk, Stanford, POEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk, R., Chen, H., Kim, C.-J., Shinn, P., Bowser, L., Chan, M. M., Chang, C. M., Dale, J. M., Hsuan, V. W., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J. M., Lin, J., Miranda, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H. L., Southwick, A., Tang, C. C., Toriumi, M., Wong, C., Wu, H. C., Yamada, K., Yu, G., Yuan, S., Davis, R. W., Theologis, A., and Ecker, J. R.

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J. R. (SSP/Salk) contributed equally to this work as PIs.

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ACCESSION	VERSION	X66016					
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SOURCE	Arabidopsis thaliana (thale cress)						
ORGANISM	Arabidopsis thaliana						
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;						
	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;						
	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.						

REFERENCE	1	(bases 1 to 2199)	Mignote-Vieux,C., Kazmaier,M., Lacroute,F. and Pompon,D.M.
AUTHORS	Unpublished		
REFERENCE	2	(bases 1 to 2199)	Pompon,D.M.
AUTHORS	Direct Submission		
TITLE	Submitted (11-MAY-1992)	D.M. Pompon, Centre de Genetique Mol du	
JOURNAL	CNRS, Avenue de la Terrasse, 91198 Gif-Sur-Yvette Cedex, FRANCE		
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DEFINITION Sequence 1 from Patent WO9321326.
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VERSION A75959.1 GI:6088149
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ORGANISM Arabidopsis thaliana
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REFERENCE 1 (bases 1 to 2114)
Kazmaier M. and Lacroute, F.
METHOD OF CLONING A DNA SEQUENCE CODING FOR A PLANT
NADPH-CYTOCHROME P450 REDUCTASE AND ASSOCIATED DNA SEQUENCES
Patent: WO 9321326-A 1 28-OCT-1993;
ORSAN (FR); KAZMAIER MICHAEL (FR)
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QY	1270 GCGCTAGCACGCTATGCTGATCTTTTGAATCTCTCTAGAAAGCTTCTCTGATTGCTCTG 1329
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RESULT 14
ECU67186 2561 bp mRNA linear PLN 06-MAR-1998
LOCUS
DEFINITION Eschecholtzia californica NADPH:ferrihemoprotein oxidoreductase


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mRNA, complete cds.
U67186
U67186.1 GI:2580498
Eschscholzia californica (California poppy)
Eschscholzia californica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
Papaveraceae; Eschscholziaceae; Eschscholzia.
1 (bases 1 to 2561)
Rosco, A., Pauli, H.H., Priesner, W. and Kutchan, T.M.
Cloning and heterologous expression of NADPH-cytochrome P450
reductases from the Papaveraceae
Arch. Biochem. Biophys. 348 (2), 369-377 (1997)
98096363
MEDLINE
9434750
PUBMED
2 (bases 1 to 2561)
Pauli, H.H. and Kutchan, T.M.
Direct Submission
Submitted (19-AUG-1996) Laboratorium fuer Molekulare Biologie,
Universitaet Muenchen, Karlstrasse 29, Munich 80333, Germany
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ORIGIN
Query Match 36.6%; Score 969.8; DB 8; Length 2561;
Best Local Similarity 68.6%; Pred. No. 2.1e-217;
Matches 1375; Conservative 0; Mismatches 607; Indels 21; Gaps 2;
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AF302497
LOCUS AF302497
DEFINITION Hybrid poplar (Populus trichocarpa x P. deltoides) NADPH-cytochrome P450 oxydoreductase isoform 2 mRNA, complete cds.
ACCESSION AF302497
VERSION AF302497.1 GI:13183563
KEYWORDS
SOURCE Populus balsamifera subsp. trichocarpa x Populus deltoides
ORGANISM Populus balsamifera subsp. trichocarpa x Populus deltoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 2493)
Ro,D.K., Ehrling,J. and Douglas,C.J.
AUTHORS Cloning, Functional Expression, and Subcellular Localization of Multiple NADPH-Cytochrome P450 Reductases from Hybrid Poplar
TITLE Plant Physiol. 130 (4), 1837-1851 (2002)
JOURNAL 12481067
PUBMED
REFERENCE 2 (bases 1 to 2493)
Ro,D.-K. and Douglas,C.
AUTHORS Direct Substitution
TITLE Submitted (05-SEP-2000) Botany, University of British Columbia,
JOURNAL 6270 University Blvd., Vancouver, British Columbia V6T 1Z4, Canada
FEATURES Location/Qualifiers
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ORIGIN

Query Match 34.7%; Score 918.6; DB 8; Length 2493;
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Db 478 AAGAGAAATTAAGAAAGAGTCTTTGGCCATTTTCTTTGGCCCATATGAGATGGTG 537
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:01:48 ; Search time 1301 Seconds
(without alignments)
12053.340 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

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9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	983.4	37.1	2114	2 AAQ51236	Aaq51236 Plant NAD
3	958.6	36.2	2558	2 AAX08520	Aax08520 Poppy cyt
4	895.4	33.8	2136	3 AAC44709	Aac44709 Arabidops
5	895.4	33.8	2136	6 ABZ12998	Abz12998 Arabidops
6	895.4	33.8	2136	8 ADA68489	Ada68489 Arabidops
7	875	33.0	2423	2 AAQ51237	Aaq51237 Plant NAD
8	859.8	32.5	2112	2 AAQ51238	Aaq51238 Plant NAD
9	849	32.0	2581	10 ADF89810	Adf89810 Triterpen
10	807.6	30.5	1863	6 AAD33078	Aad33078 Helianthu
11	807.6	30.5	1863	6 AAD26926	Aad26926 Helianthu
12	770.2	29.1	1985	12 ADJ10845	Adj10845 Recombina
13	586.4	22.1	2016	8 ADA70621	Ada70621 Rice gene
14	339.6	12.8	683	13 ADR60759	Adr60759 Cotton cd
15	272.2	10.3	609	13 ACN62895	Acn62895 Cotton ca
16	269.6	10.2	612	13 ACN62802	Acn62802 Cotton ca
17	263	9.9	555	13 ACN50810	Acn50810 Cotton an
18	257.4	9.7	638	13 ADR60436	Adr60436 Cotton cd
19	244.2	9.2	614	13 ACN51360	Acn51360 Cotton an
20	231.8	8.8	485	3 AAC35800	Aac35800 Zea may

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23	195.6	7.4	2441	10 ADB53276	Adb53276 Primary r
24	195.6	7.4	2441	10 ABT42217	Abt42217 Toxicity
25	194	7.3	2401	6 ABK63490	Abk63490 Rat seque
26	194	7.3	2401	12 ADP72624	Adp72624 Renal tox
27	193.4	7.3	349	6 ABQ85854	Abq85854 Arabidops
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29	192.8	7.3	1872	6 ABK63444	Abk63444 Rat seque
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33	192.8	7.3	3435	1 AAN81746	Aan81746 Plasmid p
34	191.4	7.2	3399	1 AAN81747	Aan81747 Plasmid p
35	191.2	7.2	2037	1 AAN70925	Aan70925 Sequence
36	191.2	7.2	3453	1 AAN81744	Aan81744 Plasmid p
37	189.2	7.1	2461	11 ACN44409	Acn44409 Mouse mRN
38	187.6	7.1	2450	1 AAN70605	Aan70605 Plasmid p
39	187.4	7.1	2457	6 ABI99690	Abi99690 Mouse isc
40	187.4	7.1	2457	12 ACF57504	Acf57504 Murine p4
41	187.4	7.1	2457	12 ADJ62862	Adj62862 Mouse p45
42	177.4	6.7	2721	4 ABL15291	Abli15291 Drosophil
43	170.4	6.4	3489	1 AAN81745	Aan81745 Plasmid p
44	169.4	6.4	3310	3 AAZ93331	Aaz93331 Partial s
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ALIGNMENTS

RESULT 1
AAX08517
ID AAX08517 standard; DNA; 2650 BP.
XX
AC AAX08517;
XX
DT 19-JUL-1999 (first entry)
XX
DE Poppy cytochrome P450 reductase.
XX
KW Opium poppy; alkaloids; cytochrome P450 reductase; morphine; codeine;
KW oripavine; thebaine; transformation; crop yield; probe; primer; ss.
OS Papaver somniferum.
XX
FH Key Location/Qualifiers
CDS 124..2175
FT /*tag= a
FT /product= "Cytochrome P450 reductase"
XX
PN WO9911765-A1.
XX
PD 11-MAR-1999.
XX
PF 28-AUG-1998; 98WO-AU000705.
XX
PR 29-AUG-1997; 97AU-00008872.
XX
PA (JOH J) JOHNSON & JOHNSON RES PTY LTD.
PI Kutchan TM, Zenk MH, Atkins DG, Fiet AJ;
XX
XX WPI; 1999-214703/18.
DR P-PSDB; AAW85680, AAW85682.
XX
PT Nucleic acid encoding cytochrome P-450 reductase from poppy.
XX
PS Claim 3; Fig 9a; 58pp; English.
XX
CC Transforming plants with a nucleic acid molecule encoding cytochrome P450
CC reductase alters the yield and/or type of alkaloids produced. In opium
CC poppies it specifically increases the yield of medically useful alkaloids
CC such as morphine, codeine, oripavine and thebaine. Sequences


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Db 1921 ATTGCTCTTTTACGTGAAGGGGAAAAGAGGAATATGTTCAACATAGATGATGGAGAAA 1980
Qy 1981 GCAACGATGTATGGAATGTATATCAGGGGACGGTTATCTCTATGTGTGTGTATGCC 2040
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Qy 2161 AGAGATGCTGTGGTATCGAATGTAGCTTGCATGCTCCCAAGTCCCTTTCTTGGCTGTGTTA 2220
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Db 2581 TTCTTGTGTTTCTTATGCTACCGAGGAGTATATTAATGATTTAGAGTTTGTAGAAA 2640
Qy 2641 AAAAAAAAAA 2649
Db 2641 AAAAAAAAAA 2649

RESULT 2
ID AAQ51236 standard; cdna; 2114 BP.
XX
AC AAQ51236;
XX
DT 25-MAR-2003 (revised)
DT 11-MAY-1994 (first entry)
XX
DE Plant NADPH cytochrome P450 reductase (ara B).
XX
KW NADPH cytochrome P450 reductase; functional complementation;
KW identification; ss.
XX
OS Arabidopsis thaliana.
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FH Key Location/Qualifiers
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XX
XX 28-OCT-1993.
XX
XX 13-APR-1993; 93WO-FR000367.
XX
XX 13-APR-1992; 92FR-00004491.
XX
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PA	(ORSA-) ORSAN.	
XX	Kazmaier M, Lacroute F, Mignotte-Vieux C, Minet M, Pompon D;	
XX	WPI; 1993-351736/44.	
DR	P-PSDB; AAR43581.	
XX	New DNA encoding plant NADPH cytochrome P450 reductase - cloned by	
PT	functional complementation in yeast, also recombinant enzyme useful in	
PT	P450 mediated bioconversion processes.	
XX	Claim 11; Fig 9; 79pp; French.	
PS		
XX		
CC	A new method for determining whether a DNA sequence encodes an NADPH	
CC	cytochrome P450 reductase involves transforming yeasts with plasmids of a	
CC	total cDNA bank of plant(s). The yeasts used in the procedure are	
CC	incapable of producing their own NADPH cytochrome P450 reductase. They	
CC	are then exposed to a cytochrome P450 inhibitor at a level which is	
CC	lethal to the yeast cells but not to cells which, because of the	
CC	transformation, now contain an active NADPH cytochrome P450 reductase.	
CC	Surviving clones are then isolated and plasmid DNA extracted. The gene is	
CC	inserted into the plasmid at a site which places it under the control of	
CC	an inducible promoter. (Updated on 25-MAR-2003 to correct PN field.)	
XX		
SQ	Sequence 2114 BP; 603 A; 400 C; 542 G; 569 T; 0 U; 0 Other;	
	Query Match 37.1%; Score 983.4; DB 2; Length 2114;	
	Best Local Similarity 71.1%; Pred. No. 1.5e-254;	
	Matches 1337; Conservative 0; Mismatches 526; Indels 18; Gaps 2;	
QY	310 ATAAATGATGAAGAAGAGGAGATGAAGTTGATCTCGTGGTAAATTAAGCTCATTATA 369	970 TTTGATATTCTCCATCTCTTGAGAAACCAATFTGTTGCTCAACAAAGAGAGCTCCACAAACCC 1029
DB	237 ATGGCTAAGGACGAGGATGATGATTTGGATTTGGGATTCGGGAAGACTAGAGTCTCTATC 236	894 ATTGCAATTCATCATCCCTGCAGAGTTGATGTTGCTGTCAGAAAGAGCTTCACACACAT 953
QY	370 TTTTGTGGTACTCAGACTGCTACTGCTGAAGGATTTGCTAAGGCATTTGGCAGAAGAAATT 429	1030 AAGTCTGTAGATACCTGTATATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACATAT 1089
DB	297 TTCTTCGGTACGACAGCTGGAACAGCTGAGGATTTGCTNAGGCATTTCCGAAAGATC 356	954 GAATCTGATCGGTCTTGGCAATCATCTCGAGTTTCGACATATCCAGGACGGGTATTACATAT 1013
QY	430 AAGGCAAAAGTACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACGCCGAG 489	1090 GAGACTGGAGATCATGTTGTTGTTATGCTGAGAACTGCGATCAAACTCTCGAGGAAGCA 1149
DB	357 AAAGCGAGATATGAAAAGCAGCAGTCAAAGTCATTTGACTTGGATGACTATGCTGCCGAT 416	1014 GAAACAGGTGACCATGTAGTGTATATGCTGAAATCATGTTGAGATAGTTGAAGAAGCT 1073
QY	490 GATGATCAATATGAAGAGAAATTAAGAAAGAGTCTTTGTTGTTTTCATGTTAGCCACT 549	1150 GGGAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTTCATTTCAATTCACACGATAAAGAGAC 1209
DB	417 GATGACAGTATGAAGAGAAATTTGAAGAGGAACTTTGGCATTTTCTGTGTGTACT 476	1074 GGAATAATTTCTTGGCCACTCTTTAGATTAGTATTTTCCATATCATCTGACAAAGGAAT 1133
QY	550 TATGGTGATGCTGAGCCTGACAACTGTCGAGATTTTACAAATGGTTCACTCAGGAA 609	1210 GGGTCAACCCAGGAGGACTCATTTACCACCTCTTTCCAGGTCCTTGACCTTACCATCT 1269
DB	477 TATGGAGATGGAGGCTACTGACAAATGCTGCCAGATTTTCAAAATGGTTTACGGAGAA 536	1134 GGTCTCCCAATTGAAAGCGCAGTGGCCCTCTTTCCCTGGTCCATGACACTTTGGGACT 1193
QY	610 CATGAAAGGGGAGTGGCTTCAGCAACTAACTTATGTTGTTTGGTTTGGTTGGTAAACCGT 669	1270 GGCCTAGCAGCTATGCTGATCTTTTGAATCTCTTAGAAAGGCTTCTCTGATTGCTCTG 1329
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QY	670 CAATACAGCATTTCAACAGATCGGTTAGTGTGATGTCGATGAGCAACTCGTAAACAGGT 729	1330 TCCGCTCATGCTCTGTACCCAGTGAAGCAGAGATTTGGCTTTTGTGTCATCACCTCTG 1389
DB	597 CAATATGAACATTTAATAAGATCGGGATAGTTCTTGTATGAAGATTTATGTAAGNAAGGT 656	1254 GCGGCTATGCTCCACTGAACCAAGCGAAGCCGAGAACTTTAAGCACCTGACATCACCTGAT 1313
QY	730 GCAAAGCGCATTTGTTCAAGTGGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTT 789	1390 GGAAGAATGAGTATTTCAAAATGGGTAGTTGGAAGTCCAGAGGAGTCTTTTGGAGATCATG 1449
DB	657 GCAAAGCGCTTTATTTGNAAGTGGTCTAGGAGATGATGATCAGAGCATTTGAGGATGATTTT 716	1314 GGAAGAGTGAAGTACTCAATGGATTTGTCAGAGTTCAGAGAGTCTTTTAGAGGTGATG 1373
QY	790 ACTGCTTGGCGAGAAATTTGTTGGACTGAAATGGATCAGTTGCTCAAAGATGAGGATGCT 849	1450 GCGAGTTTCCCATCAGCAAAACCCCTCTTGTGTGTTCTTTGCTGCAGTAGCCCTCGC 1509
DB	717 AATGCTCGGAAGAAATCACTATGCTGAGCTAGACAAAGCTCTCAAAGACGAGGATGAT 776	1374 GCTGCTTTTCCATCTGCAAAACCCCACTAGGTGATTTTGTGCAATAGCTCTCGT 1433
QY	850 GCTCCTTCAGTGGCTACACCGTATATGCTACTGTTCTCTGTAATACAGGTTAGTATCAC 909	1510 TTACCGCTCTGATATATTTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAATTCTAT 1569
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QY	910 GAAACTACGGTCCGGCTCTGGATGATAAACAATAAAATCTGCTAAACGGCGATTTTGCA 969	1570 GTGAGTGTGCTTTAGTATATGTCAAAGCCCTACCGAAGGTTTCACCGAGGAGTGTGT 1629
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Db 1387 GCATCCGATCCAAAGGAAGCGAGCGACTAAGGTATCTTCGCTCTCTGCTGGGAAGGAC 1446
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Db 1507 CCATCAGCAAGGCTCCAAATGGGTTTCTTTGACAGCTAGCTCTCGTTGCTGCCA 1566
Qy 1519 CGATACATTTCTATCTCATCTCTCTTAAGTTTGTCTCCCAAGAAATTCATGTGACGTGT 1578
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Qy 1639 ATGAAGCATCAGTTCTCTCAGGA-----TAGCTGGGCTCCTATTTTTT 1680
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Qy 1681 GTTCGAAGCTCAAACTTCAAGTTACAGCTGACCCCTCAACTCCAATTATCATGTGGGA 1740
Db 1747 GTCAGGCAATCCAACTTCAAACTTCCTGCTGATTTCTACAGTACCAATTAATGATTGT 1806
Qy 1741 CTTGTTACAGGGTTAGTCTCTTTTCAGAGATTTCTCAGGAAGAATGGCCCTCAAGGA 1800
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Qy 1801 AATGGTGCTCAACTGGCCCGAGCTGCTCTTTTTCGATGTAGGAATCGTAATATGGAC 1860
Db 1867 TCTGGTGTAGAAATGGGACCGCTATCCTCTCTTTGGATGCAGAACACAGATGGAT 1926
Qy 1861 TTCAATTTAAGACGAACTAAACAACCTTCGTGGAACGAGGAGTCAATTCGGAGCTAGTT 1920
Db 1927 TACATATATGAAGAGGAGCTAAACAACCTTGTGAAAGAGGAGCTATCTCCGAAGTTGTT 1986
Qy 1921 ATTGCCCTTTTCAGTGAAGGGGAAAGAGGAATATGTTCAACATAAGATGATGGAGAA 1980
Db 1987 GTTGTCTTCTCAGTGAAGGAGTCAACAGGAATACGTACAAATAAATGGCGGAGAG 2046
Qy 1981 GCAACGGATGATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGATGCC 2040
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Qy 2101 ATGGAATCATCTGCTCCGAGCTGCAGTAAGAACTCCAAGTTGAAGACGATATCTTA 2160
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Qy 2161 AGAGATGCTCTGGTGATCGAATGT 2183
Db 2227 CGTGATGTGTGGTGAATGATTTT 2249

RESULT 4
AAC44709
ID AAC44709 standard; DNA; 2136 BP.

XX AC AAC44709;
XX AC
XX AC
DT 18-OCT-2000 (first entry)
XX Arabidopsis thaliana DNA fragment SEQ ID NO: 43838.
DE
XX

KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway; metabolic pathway;
XX promoter; termination sequence; ss.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-00301439.
XX
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PR 04-OCT-1999; 99US-0157117P.
PR 05-OCT-1999; 99US-0157753P.
PR 07-OCT-1999; 99US-0157865P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159294P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159329P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 14-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161922P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 33.8%; Score 895.4; DB 3; Length 2136;
Best Local Similarity 67.3%; Pred. No. 8.7e-231;
Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;

QY 206 TCATTATGGTCACAACCTGTAGCTTCAATGCTGATTGAGTTGGTTCTTCGCAATGATGA 265
DB 161 TGATTGTTACCACTTCCATTGCTTCTTATTGTTGTCATCGTTATGCTGTTTGGAGGA 220
QY 266 AATCTTTCGTTCTTCAATCAAAACCTATTGAACTTATAAACCAATAATTGATAAAGAAG 325
DB 221 GATCCGGTTCTGGGAATTCAAAACGTGTCGAGCTCTTAAGCCTTTGGTTATTAAAGCCTC 280
QY 326 AAGAGGAGATTGAAGTTGATTCCTGGTAAATTAAGCTCACTATATATTTTGGTACTCAGA 385
DB 281 GTGAGGA---AGAGATTGATGATGGCGGTAAGAAAGTTACCACTCTTTTCGGTACACAAA 337
QY 386 CTGGTACTGCTGAAGGATTTGCTAAGGCATTTGGCAGAGAAGAAATTAAGGCAAGATACAAGA 445
DB 338 CTGGTACTGCTGAAGGTTTTCGAAAGGCTTTAGGAGAAGAAAGCTAAAGCAAGATATGAAA 397
QY 446 AAGCAGTTCTTAAAGTAGTTGACCTGGATGACTATGCACCGGAGGATGATCAATATGAAG 505
DB 398 AGACCAGATTCAAAATCGTTTGATTTACCGCGCTGATGATGATGATGATGATGAGG 457
QY 506 AGAAATTAAGAAAGAGTCTTTTGGTGTCTTTTTCATGCTAGCCACTTATGGTGGTGAGC 565
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Db 458 AGAAATTGAAGAAAGAGATGTGGCTTTCTTCTTTAGCCACATATGGAGATGGTGAGC 517
Qy 566 CAATGCAATGTGCGAGATTTTACAAATGGTTTCACTCAGGAACATGAAGAGGGAGAGT 625
Db 518 CTACCGACAATGCGAGAGATTTCAAAATGGTTTCCCGAGGGGAATGACAGAGGAGAAT 577
Qy 626 GCGTTGAGCAACTAACTTATGGTGTGTTTGGTTGGGTAAACCGTCAATACAGGACATTTCA 685
Db 578 GCGTTTAAAGAACTTTGAAGTATGGAGTGTGTTGGATTAGGAAACACACAATATGACATTTTA 637
Qy 686 ACAAGATCGGGTAGATGTGGATGAGCAACTCGGTAAACAAGGTGCAAAAGCGCATTTGTC 745
Db 638 ATAAGGTTGCAAGTTGTAGATGACATTTCTGTGCAACAAAGGTGACAGCGTCTTTGTAC 697
Qy 746 AAGTGGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTTACTGCTTGGCGAGAAT 805
Db 698 AAGTGGTCTTGGAGATGATGACCAAGTGTATTTGAAGATGACTTTTACCGCTTGGCGAGAAG 757
Qy 806 TGTGTTGGACTGAATTTGGATCAGTTGCTCAAGATGAGGATGCTGCTTCAAGTGCGTA 865
Db 758 CATTTGGGCCGAGCTTGATACAATACTAGGGAAGAAGGGGATACAGCT---GTGCGCA 814
Qy 866 CACGCTATATTGCTACTGTTCCCTGAATACAGAGGTAGTATTACAGAACTACGGTGC CGG 925
Db 815 CACATACACTGCGAGTGTGTTAGATAACAGATTTCTATTACGACTCTGAAGATGCCA 874
Qy 926 CTCGGATGATAAACACATAAATACTGCTAAACGGCGATGTTGCAATTTGATATTTCCATC 985
Db 875 AATTCAATGATATAAATCATGGCAATGGGAATGGTTACAGTGTGTTGATGCTCAACATC 934
Qy 986 CTTTGCAGAACCATTTGCTCAACAAAGAGAGCTCCACAACCAAGTCTGATAGATCCT 1045
Db 935 CTTTACAAAGCAAAATCGCTGTTTAAAGGGAGCTTCATCTCCGAGTCTGATCGTTCTT 994
Qy 1046 GTATACATCTGGAGTTTCGACATATCAGGCTTTCCCTTACATATGAGACTGGAGATCATG 1105
Db 995 GTATCAATTTGGAAATTTGACATTTGCTGGAAGTGGACTTACGTTATGAACTGGAGATCATG 1054
Qy 1106 TTGGTGTATTGCTGAGAACTGCGATGAAACTCTCGAGGAAGCAGGGAAGCTGTTGGGTC 1165
Db 1055 TTGGTGTACTTTGTGATAACTTAAGTGAAACTGTAGATGAAGCTTTAGATTGCTGGATA 1114
Qy 1166 AACCCCTGGATTTGCTGTTTTCATTTACACCGGATTAAGAGACGGGTCAACCCAGGGA 1225
Db 1115 TGTCACTGTATCTTATTTCTCACTTCACTGAGCTGAAAGAGAGCGGACCAATCAGCA 1174
Qy 1226 GCTCATTTACCACCTCTTTCCAGAGTCTTTCACCTTACGATCTGCCCTAGCAGCTATG 1285
Db 1175 GCTCAGTGCCTCTCCCTTCCCA---CCTTGGAACTTGAGAACAGCGCTTACAGATATG 1231
Qy 1286 CTGATCTTTTGAATCTCTTAGAAAGCTTCTCTGATTTGCTGTCTGCTCATGCAATCTG 1345
Db 1232 CATGCTCTTTTGGTCTTCCAAAGAAAGTCTGCTTTAGTTGGTGTGGCTCATGCACTG 1291
Qy 1346 TACCCAGTGAAGCAGAGAGATGGCTTTTGTGTCATCACCTCTGGGAAGAAGTACTT 1405
Db 1292 ATCTTACCGAAGCAGAACGATTAACACACCTTGTCTCACCTGTGGAAGGATGAATAT 1351
Qy 1406 CAAAATGGGTAGTTGGAAGTCAGAGGATCTTTTGGAGATCATGGCGGAGTTTCCATCAG 1465
Db 1352 CAAAGTGGGTAGTAGAGTCAAGAACTCTTCTGAGGTGATGGCGGAGTTTCTTCTCAG 1411
Qy 1466 CAAAACCCCTCTTGTGTTGTTCTTTGCTGAGTAGCCCTCGCTTACCGCCCTCGATACT 1525
Db 1412 CCAAGCCACCACTTGTGTCTTCTCGCTGGAGTTGCTTCCAAAGGTTGCGAGCTTAGGTTCT 1471
Qy 1526 ATTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAAATTCATGTCAGTGTGCTTAG 1585
Db 1472 ATTGATATCATCATGCCCAAGATGCTGAAATAGAAATTCAGTCAATGTCAGCTGG 1531
Qy 1586 TATATGTTCAAAGCCCTTACCGGAAGGGTTTCCCGAGAGGTGTGTTCCACATGGATGAAGC 1645
Db 1532 TTTATGAGAAATGCCAACTGGCAGGATTCATAAGGGAGTGTGTTCCACTTGGATGAAGA 1591

Qy 1646 ATGCAAGTTCTCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAAAGCT 1690
Db 1592 ATGCTGTGCTTTACGAGAAGAGTGAAAACCTGTTCTCGCGCGCATATTTGTAGGCAAT 1651
Qy 1691 CAACTTCAAGTTACAGCTGACCCCTCAATCCAAATATCATGTTGGGACCTGTGACAG 1750
Db 1652 CCAACTTCAAGCTTCTCTGATTTAAGGTACCGATCATGATCGGTCCAGGGACTG 1711
Qy 1751 GGTTAGCTCCTTTTCAGAGGATTTCTCGAGAAAGAAATGGCCCTCAAGGAAAATGGTGCTC 1810
Db 1712 GATTAGCTCCATTCAGAGGATTTCTTCAGAAAGACTAGCGTTGGTAGAATCTGGTGTG 1771
Qy 1811 AACTTGGCCAGAGTGTCTTTTTCGGATGTAGGAATCGTAATATGGAATCTTCAATTTATG 1870
Db 1772 AACTTGGGCACTAGTGTGTTTCTTTGGATGCAGAAACCGTAGAATGGATTTTCATCTACG 1831
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Db 1832 AGAAGAGCTCCAGCGATTTGTTGAGGTGGTCTCTCCAGAGCTTAAGTGTGCGCTTCT 1891
Qy 1931 CACGTGAAGGGGAAAGAGGAATATGTTTCAACATAAGATGATGGAGAAAGCAACGGATG 1990
Db 1892 CTGCTGAAGAGCCCAACCAAGAAATACGTACAGCAACAAGATGATGGACAAGGCTTCTGATA 1951
Qy 1991 TATGGAATGTATATCAGGGACGGTTATCTCTATGTGTGTGATGATCCAGGGAATGG 2050
Db 1952 TCTGGAATATGATCTCTCAAGGAGCTTATTTATATGTTTGTGTGACGCCAAAGGCAATG 2011
Qy 2051 CCAGAGATCTCCATCGCAGCTTTCATACCATTTGCCAAGAACAGGACCCATGGAAATCAT 2110
Db 2012 CAAAGATGTTTACAGATCTCTCCACAATAGCTCAAGAACAGGGGTCAATGGATTCAA 2071
Qy 2111 CTGCTGCCAAGCTGCAGTAAAGAACTCCAAAGTTGAAGAACGATATCTAAGAGATGTCT 2170
Db 2072 CTAAGCAGAGGGCTTCGTGGAAGAACTCTGCAAAAGAGTGGAAAGATATCTTAGAGATGTAT 2131
Qy 2171 GGTGA 2175
Db 2132 GGTAA 2136

RESULT 5

ABZ12998
ID ABZ12998 standard; DNA; 2136 BP.

XX ABZ12998;

DT 21-JAN-2003 (first entry)

XX Arabidopsis thaliana stress regulated gene SEQ ID NO 803.

DE Arabidopsis thaliana; plant; gene; stress; transgenic; ds.

XX Arabidopsis thaliana.

XX WO200216655-A2.

XX 28-FEB-2002.

PD 24-AUG-2001; 2001WO-US026685.

PF 24-AUG-2000; 2000US-0227866P.

XX 26-JAN-2001; 2001US-0264647P.

PR 22-JUN-2001; 2001US-0300111P.

XX (SCRI) SCRIPPS RES INST.

PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX Harper JF, Kreps J, Wang X, Zhu T;

XX WPI; 2002-304127/34.

PT Identifying a stress condition to which a plant cell has been exposed and
XX producing plants with increased tolerance to these abiotic stresses.

PS Claim 144; SEQ ID NO 803; 577bp + Sequence Listing; English.

XX The invention relates to identifying a stress condition to which a plant
CC cell has been exposed, comprising: (a) contacting nucleic acid
CC representative of expressed polynucleotides in the plant cell with an
CC array or probes representative of the plant cell genome; and (b)
CC detecting a profile of expressed polynucleotides in the plant cell
CC characteristic of a stress response. The method is useful in the
CC production of transgenic plants, cells and seeds and in producing plants
CC with increased tolerance to abiotic stress. The present sequence is that
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used
CC in methods of the invention. Note: The sequence data for this patent is
CC not represented in the printed specification but is based on sequence
CC information supplied to Derwent by the European Patent Office

XX Sequence 2136 BP; 595 A; 424 C; 519 G; 598 T; 0 U; 0 Other;

Query Match 33.8%; Score 895.4; DB 6; Length 2136;

Best Local Similarity 67.3%; Pred. No. 8.7e-231;

Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;

Qy 206 TCATTATGGTCAACACTGTAGCTTCAATGCTGATGGAATTGGTTCTTCGCGATGATGA 265
Db 161 TGATTGTTACACTTCCTCAATGCTGTTCTTATGCTGTCATGCTATGCTCGTTGGAGGA 220
Qy 266 AATCTTCGCTTCTCAATCAAACTTATGAACTTATAAACCATAAATTGATAAAGAG 325
Db 221 GATCCGGTTCGGAATTCAAAACGTCGAGCGCTTAAAGCCCTTGGTTATTAAAGCCTC 280
Qy 326 AAGAGGAGATTGAAGTTGATCTCGTAAATTAAGCTCACTATATTTTGGTACTCAGA 385
Db 281 GTAGGA---AGATTGATGATGGCGGTAAAGATTACATCTTTTCGGTACAAA 337
Qy 386 CTGCTACTGCTGAAGGATTTGCTAAGGCATTGGCAGAGAAATTAAGCCAAAGTACAAGA 445
Db 338 CTGCTACTGCTGAAGGTTTTCGAAAGGCTTTAGGAGAAGAGCTAAAGCAAGATATGAA 397
Qy 446 AAGCAGTTGTTAAAGTATGTCCTGATGACTATGACGCGGAGGATGATCAATATGAAG 505
Db 398 AGACCAGATTCAAAATCGTTGATTTGGATGATTAACGCGCTGATGATGATGATGAGG 457
Qy 506 AGAAATTAAGAAAGAGCTTTGCTGTTTTCATGTTAGTACCTATGTTGGTGGTGGAGC 565
Db 458 AGAAATTAAGAAAGAGATGTCGCTTCTCTTCTTAGCCATATGAGAGTGGTGGAGC 517
Qy 566 CAACGTGCAATGCTGCGAGATTTTACAAATGGTTTCACTCAGGAACATGAAGGGGAGAGT 625
Db 518 CTACCGAATGCGAGGAGATTTACAAATGGTTTCAACGAGGGGAGATGACAGAGGAGAT 577
Qy 626 GGCTTACGAACTAACTTATGTTGTTTGGTTGGGTAAACCGTCAATACGAGCATTTCA 685
Db 578 GGCTTAAAGAACTTGAAGTATGAGTGTGTTGGATTAGGAAACAGACAATATGACATTTA 637
Qy 686 ACAAGATCGCGGTAGATGTCGATGAGCACTCCGTAACAGGTGCAAGCGCATTTGTC 745
Db 638 ATAAGGTTGCAAGTTGTAGATGACATTCCTGTCGAAACAGGTGACAGCGCTTTGTAC 697
Qy 746 AAGTGGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTTACTGCTTGGCGAGAAT 805
Db 698 AAGTGGTCTTGGAGATGATGACGAGTGTATTGAAGTACTTACCGCTTGGCGAGAG 757
Qy 806 TGTGTGGAATGATGATGATGCTTCAAGATGAGGATGCTGCTCTTCAAGTGGCTA 865
Db 758 CATTTGGTGGCCGAGCTTGTATACAACTACTGAGGGAAGAGGGGATACAGCT---GTTGCCA 814
Qy 866 CACCGTATATGCTACTGTTCTCTGAATACAGGCTAGTATTACGAAACTACGGTCCGG 925
Db 815 CACCATACATCGAGCTGTGTTAGAAATACAGAGTTTCTATTACGACTCTGAAGATGCCA 874
Qy 926 CTCTGGATGATAAACACATAAATACTGCTAAACGGCGATGTTGCAATTTGATATTCTCCATC 985

Db 875 AATTCAATGATATAAATCGCAATGGGAATGGTATACACTGCTGTTGATGCTCAACATC 934
Qy 986 CTTGCGAAGCAATGTTGCTCAACAAAGAGAGCTCCAAACCCCAAGCTCTGATAGATCCT 1045
Db 935 CTTTACAAAGCAATGTCGCTGTTTAAAGGGAGCTTCACTACCTCCGAGCTCTGATCGTTCT 994
Qy 1046 GTATACATCTGGAGTTCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATG 1105
Db 995 GTATCCATTTGGAATTTGACATTTGCTGGAAGTGGACTTACGTATGAAACTGGAGATCATG 1054
Qy 1106 TTGCTGTTTATGCTGGAACCTGCGATGAAACTGTGCGAGGAAGCAGGAAGCTGTTGGGTC 1165
Db 1055 TTGCTGTTTATGCTGTAACCTTAAGTGAACCTGTAGATGAAGCTCTTATAGATTGCTGGATA 1114
Qy 1166 AACCCCTGGATTTGCTGTTTCAATTCACAGGATAAAGAGAGCGGTCAACCCAGGGAA 1225
Db 1115 TGTACCTGTATCTTATTTCTCACTTCAACGCTGAAAAGAGAGCGGCACCAATCAGCA 1174
Qy 1226 GCTCATTTACCACTCTCTTCCAGGTCCTTGCACCTTACCATCTGCCCTAGCACGCTATG 1285
Db 1175 GCTCATGCTCTCTCTCTCTCCCA---CCTTGAACCTTGAAGACAGCGCTTACAGATATG 1231
Qy 1286 CTGATCTTTTGAATCTCTCTAGAAAGCTTCTCTGATTTGCTCTGCTCGCTCATGCACTG 1345
Db 1232 CATGCTCTTTGAGTCTCTCAAGAGAGTCTGCTTTAGTTGGTGGCTGCTCATGCACTG 1291
Qy 1346 TACCCAGTGAAGCAGAGATTCGCGCTTTTGTGTCATCACCTCTGGGAAAGAGATGATTT 1405
Db 1292 ATCTTACCGAAGCAGAGATTAACACACCTTCTTCACTGCTGGAAGAGATGATTT 1351
Qy 1406 CAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGGCCGAGTTCCTCATG 1465
Db 1352 CAAAGTGGGTAGTAGAGATCAAGAGATCTACTTGAGGTGATGGCCGAGTTCCTTTAG 1411
Qy 1466 CAAAACCCCTCTTGTGTGTTCTTTGCTGAGTAGCCCTCTGCTTACCCCTCGATACT 1525
Db 1412 CCAAGCCACCACTTGTGTCTTCTCGTGGAGTGTCTTCCCAAGGTGTCAGCCCTAGTTC 1471
Qy 1526 ATTCTATCTCATCTCTCTTAAGTTTGTCTCCCTCAAGAAATTCATGTGACGTGTGCTTAG 1585
Db 1472 ATTCGATATCATCATGCCCAAGATTTGCTGAAACTAGAAATTCACGTACATGTGCACTG 1531
Qy 1586 TATATGCTCAAGCCCTACCGAAGGTTTCAACGAGAGGTGCTCGACATGATGAAGC 1645
Db 1532 TTTATGAGAAATGCCAATGCGCAGATTCATGAAGGAGTGTGTTCCACTTTGGATGAAGA 1591
Qy 1646 ATGCACTCTCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAACGT 1690
Db 1592 ATGCTGTGCTTACGAGAAGAGTGAACCTGTTCTCGCGCCGATATTTGTTAGGCAAT 1651
Qy 1691 CAACCTTCAAGTTACAGCTGACCCCTCAACTCAATTCATGTTGGGAGCTGCTGTTAGCAG 1750
Db 1652 CCAACTTCAAGCTTCTCTGATTTCTAAGTACCGATCATCATGATCGGTCCAGGGAGCTG 1711
Qy 1751 GGTACTCTCTTTCAGAGGATTTTCAGAGAAAGATGSCCTCAAGGAAATGTTGCTC 1810
Db 1712 GATTGCTCATTCAGAGATTCCTTCAGAAAGACTAGCGTTGGTAGAATCTGGTGTG 1771
Qy 1811 AACTTGGCCACAGCTGCTCTTTTCGGATGTAGGAATCGTAAATATGGAATCTCATTTATG 1870
Db 1772 AACTTGGCCACAGTTTGTCTTCTTGGATGCAGAACCGTAGAATGATTTTCATCTACG 1831
Qy 1871 AAGACGAATAAACACTTCTGTTGGAACGAGGAGTCAATTTCCGAGCTAGTATTATTCCTTTT 1930
Db 1832 AGGAAGAGCTCCAGCGATTTGTTTGAAGTGGTCTCTCCGACAGCTAAAGTGTGCGCTTCT 1891
Qy 1931 CACGTGAAGGGGAAAGAGGAATATGTTCAACATAAGATGATGGAGAAAGCAACGATG 1990
Db 1892 CTCGTGAAGGACCCCAAGAAATACGTACGCAAGATGATGGACAGGCTTCTTGATA 1951
Qy 1991 TATGGAATGTGATATCAGGGGAGCGGTATCTCTATGTTGTGTTGATGCCAAGGAATGG 2050

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Db 1952 TCTGGAATATGATCTCTCAAGSAGCTTATTTATATGTTTGTGTGACGCCAAAGGCATGG 2011
QY 2051 CCAGAGATGTCCTCGACGCTTGCATACCATTCGCCAAGAAACAGGACCCCATCGAATCAT 2110
Db 2012 CAAGAGATGTTACAGATCTCTCCACAAATAGCTCAAGAACAGGGGTCAATGGATCAA 2071
QY 2111 CTCTGCCGAAGTGCAGTAAAGAACTCCAAAGTTGAAGAACGATATCTAAAGAGATGTCT 2170
Db 2072 CTAAGAGCAGAGGGCTTCGTGAAGAACTCTGCAACCGAGTGAAGATATCTTAGAGATGTAT 2131
QY 2171 GGTGA 2175
Db 2132 GGTA 2136

RESULT 6
ADA68489
ID ADA68489 standard; DNA; 2136 BP.
XX
AC ADA68489;
XX
DT 20-NOV-2003 (first entry)
XX
DE Arabidopsis thaliana gene, SEQ ID 605.
XX
KW Plant; bacterial infection; fungal infection; viral infection; ds.
XX
OS Arabidopsis thaliana.
XX
PN W02003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 6; SEQ ID NO 605; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2136 BP; 595 A; 424 C; 519 G; 598 T; 0 U; 0 Other;

Query Match 33.8%; Score 895.4; DB 8; Length 2136;
Best Local Similarity 67.3%; Pred. No. 8.7e-231;
Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;

QY 206 TCATTATGGTCACAACGTAGCTTCAATGCTGATGGATTTGGTTCTTTCGGCATGTATGA 265
Db 161 TGATTGTTACCACTTCATTGCTGTTCTTATTGGTTGCATCGTTATGCTGTTTGGAGGA 220
QY 266 AATCTTCGCTTCTCAATCAAAACCTATTGAAACCTTATAAACCAATAATTGATAAAG 325
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Db 221 GATCCGGTCTCGGAATTCAAAACCGTGTGAGCCTCTTAAGCCTTTGGTTATTAAGCCTC 280
QY 326 AAGAGGAGATTTGAAGTTGATCTCTGGTAAATTAAGCTCACTATATTTTGGTACTCAGA 385
Db 281 GTGAGGA---AGAGATTTGATGATGGCGGTAAAGAAAGTTTACCATCTTTTTTCGGTACAAA 337
QY 386 CTGGTACTCTCAAGGATTTGCTAAAGGCATTTGGCAGAGAAAATTAAGGCAAAAGTACAAGA 445
Db 338 CTGGTACTCTCAAGGTTTTTGCANAAGCCTTTAGGAGAAGCAAGCAAGATATGAAA 397
QY 446 AAGCAGTTGTTAAAGTAGTTGACCTCGGATGACTATGACAGCCGAGGATGATCAATATGAAG 505
Db 398 AGACCAGATTCAAAATCGTTGATTTTGGATGATTAACGCGGTGATGATGATGATGAGG 457
QY 506 AGAAATTAAGAAAGAGTCTTTTGGTGTCTTTTTCATGTGTAGCCACTTATGTGTGTTGAGC 565
Db 458 AGAATTTGAAGAAGAGGATGTGGCTTTCTTTCTTAGCCACATATGGAGATGGTGAGC 517
QY 566 CAACTGACAAATGCTCGAGATTTTACAAATGGTTTCACTCAGGAACATGAAAAGGGAGAGT 625
Db 518 CTACCGACAAATGCAGCGAGATTTCTACAAATGGTTTACCGAGGGGAATGACAGAGGAGAAT 577
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Db 578 GGCCTTAAGAACTTGAAGTATGGAGTGTGTTTGGATTTAGGAAACAGACAATATGAGCATTTTA 637
QY 686 ACAAGATCCGGTGTAGATGTGGATGAGCAACTCGGTAACAAGGTGCAAAAGCGCATTTGTC 745
Db 638 ATAAGTTGCCAAAGTTGTAGATGACATTTCTTGTGCAACAGGTGCAAGCGTCTTGTATC 697
QY 746 AAGTGGGGCTCGGTGACGATGATCAATGCAATGAAGATGATTTTACTGCTTGGCGAGAAT 805
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Db 758 CATTTGGCCCCGAGCTTTGATACAATACTGAGGGAAGAGGGGATACAGCT---GTTGCCA 814
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Db 875 AATTCAATGATATAAACATGCGAAATGGGAATGGTTTACACTGTGTTTGTGATGCTCAACATC 934
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Db 995 GTATCCATTTGGAAATTTGACATTTGCTGGAAGTGGACTTACGTTATGAACTGGAGATCATG 1054
QY 1106 TTGGTGTATTGCTGAGAACTCGCATGAAACTGTGTCGAGGAAGCAGGGAAGCTGTTGGGTC 1165
Db 1055 TTGGTGTACTTTGTGATAACTTAAAGTGAACCTGTAGATGAAGCTCTTAGATTGCTGGATA 1114
QY 1166 AACCCCTGGATTTGCTGTTTTCNAATTCACCGGTAAGAAGACGGGTCAACCCAGGGAA 1225
Db 1115 TGTCACTGTATACTTATTTTCTCACCTTCACGCTGAAAAGAGACGGCACCAACATCAGCA 1174
QY 1226 GCTCATTTACCACTCTCTTTCCAGAGTCTTTGACACCTTTACGATCTGCGCTAGCACGCTATG 1285
Db 1175 GCTCACTGCTCTCTCCCTTCCCA---CCTTGGCAACTTTGAGAACAGCGCTTACACGATATG 1231
QY 1286 CTGATCTTTTGAATCTCTCTAGAAAGGCTTCTCTGATTTGCTCTGTCGCGCTCATGCACTG 1345
Db 1232 CATGTCTTTTGAAGTTCTCCAAAAGAGTCTGCTTTTAGTTGCGTTGGCTGCTCATGCACTG 1291
QY 1346 TACCCAGTCAAGCAGAGAGATTCGCGCTTTTGTGTCATCACCTCTGCGGAAAGAAATGAGTATT 1405
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Db 1292 ATCTACCGAAGCAGAACGATTAAACACACCTTGCTTCACTCGTGGAAAGGATGATATT 1351
 Qy 1406 CAAATGGGTAGTTGGAGTGCAGAGGAGTCTTTTGGAGATCATGGCCGAGTTTCCATCAG 1465
 Db 1352 CAAAGTGGGTAGTAGAGTCAAGAAAGTCTACTTGGAGTGTGAGTGGCCGAGTTTCCATCAG 1411
 Qy 1466 CAAAACCCCTCTTGTGTGTCTTTTCTGCTGAGTAGCCCTCGCTTACCGCTCGATACT 1525
 Db 1412 CCAAGCCACCATTTGTGTCTTCTTCTGCTGAGTGTCTCAAGTGTGACCTAGTGTCT 1471
 Qy 1526 ATTCTATCTCATCTCTCCCTAAGTTTGTCTCCCTCAAGAAATTCATGTGACGTGTCTTAG 1585
 Db 1472 ATTCTATCTCATCTCCCTAAGTTTGTCTCCCTCAAGAAATTCATGTGACGTGTCTTAG 1531
 Qy 1586 TATATGTCTCAAGCCCTTACCGAAGGTTTCCAGGAGGTGTTCGACATGATGAAGC 1645
 Db 1532 TTTATGAAATGCCAACTGGCAGGATTCATAGGAGGTGTTCACCTTGGATGAAGA 1591
 Qy 1646 ATGAGTCTCTCAGGA-----TAGCTGGGCTCCTATTTTTGTTCGAACGT 1690
 Db 1592 ATGCTGTGCTTACGAGAGAGTGAACCTGTTCTCGGCGCGATATTTGTTAGGCAAT 1651
 Qy 1691 CAACTTCAAGTTACAGCTGACCCCTCAACTCAATATATCATGTGGGACCTGGTACAG 1750
 Db 1652 CCAACTTCAAGCTTCTCTCTGATTCTAAGGTACCGATCATCATGATCGTCCAGGGACTG 1711
 Qy 1751 GGTAGCTCTTTCAGAGGATTTCTCGAGAAAGATGGCCCTCAAGGAAATGGTCTC 1810
 Db 1712 GATTAGCTCATTACAGAGGATTCCTTCAGGAAAGACTAGCGTTGGTAGAATCTGGTGTG 1771
 Qy 1811 AACTTGGCCCGACGAGTCTCTTTTCGATGTAGGAATCGTAATATGGAATTCATTATG 1870
 Db 1772 AACTTGGCCCATCAGTTTGTCTTTGGATGCAAGAACCGTAGAATGGATTTCATCTAG 1831
 Qy 1871 AAGACGAATTAACAATCTCGTGGACGAGGATCTATTCGGAGCTAGTTATTGCTTTT 1930
 Db 1832 AGAAGAGCTCCAGCGATTTGTTGAGAGTGGTCTCTCGCAGAGCTAAGTGTGCTCTCT 1891
 Qy 1931 CAGTGAAGGGAAAGAGGATATGTTCAACATAGATGATGGAGCAACGAGATG 1990
 Db 1892 CTGTAAGAGCCCAAGAAATACGTACAGCAAGATGATGGACAGGCTTCTGATA 1951
 Qy 1991 TATGGAATGTGATATCAGGGGCGGTTATCTCTATGTGTGTGTGATGCCAAGGGAATG 2050
 Db 1952 TCTGGAATATGATCTCTCAGGAGCTTATTTATATGTTGTGTGACCCAAAGGATGG 2011
 Qy 2051 CCAGAGATGCCATCGACGCTTCATACCATTCCTCCCAAGAACAGGACCCATCGAATCAT 2110
 Db 2012 CAAGAGATGTTTCAAGATCTCTCCACATAGCTCAAGAACAGGGGTCAATGGATTCAA 2071
 Qy 2111 CTGCTCCGAGCTGCAGTAAGAAATCCCAAGTTGAAACCATATCTAAGAGATGCT 2170
 Db 2072 CTAAAGCAGGGGCTTCGTGAAGAAATCTGCAACGAGTGGAGATATCTTAGAGATGAT 2131
 Qy 2171 GGTGA 2175
 Db 2132 GGTAA 2136

RESULT 7
 AAQ51237
 ID AAQ51237 standard; cdna; 2423 BP.

AC AAQ51237;

XX 25-MAR-2003 (revised)

DT 11-MAY-1994 (first entry)

XX Plant NADPH cytochrome P450 reductase (ara C).

DE NADPH cytochrome P450 reductase; functional complementation;

XX identification; 88.

KW

XX

OS Arabidopsis thaliana.
 XX
 FH Key Location/Qualifiers
 CDS 131..2269
 FT /tag= a
 FT /product= "NADPH cytochrome P450 reductase."
 FT misc_difference 374..376
 FT /tag= b
 FT /transl_except= CGT encodes Lys.
 FT misc_difference 410..412
 FT /tag= c
 FT /transl_except= CGT encodes Lys.
 FT misc_difference 434..436
 FT /tag= d
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 FT misc_difference 518..520
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 FT /transl_except= AGA encodes Lys.
 FT misc_difference 1684..1686
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 FT misc_difference 1763..1765
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 FT misc_difference 1778..1780

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XX XX
PD 28-OCT-1993.
XX XX
XX 13-APR-1993; 93WO-FR000367.
XX XX
PR 13-APR-1992; 92FR-00004491.
XX XX
PA (ORSA-) ORSAN.
XX XX
PI Kazmaier M, Lacroute F, Mignotte-Vieux C, Minet M, Pompon D;
XX XX
DR WPI; 1993-351736/44.
DR P-PSDB; AAR43582.
XX XX
PT New DNA encoding plant NADPH cytochrome P450 reductase - cloned by
PT functional complementation in yeast, also recombinant enzyme useful in
PT P450 mediated bioconversion processes.
XX XX
PS Claim 11; Fig 10; 79pp; French.
XX XX
CC A new method for determining whether a DNA sequence encodes an NADPH
CC cytochrome P450 reductase involves transforming yeasts with plasmids of a
CC total cDNA bank of plant(s). The yeasts used in the procedure are
CC incapable of producing their own NADPH cytochrome P450 reductase. They
CC are then exposed to a cytochrome P450 inhibitor at a level which is
CC lethal to the yeast cells but not to cells which, because of the
CC transformation, now contain an active NADPH cytochrome P450 reductase.
CC Surviving clones are then isolated and plasmid DNA extracted. The gene is
CC inserted into the plasmid at a site which places it under the control of
CC an inducible promoter. (Updated on 25-MAR-2003 to correct PN field.)
XX XX
SQ Sequence 2423 BP; 674 A; 497 C; 552 G; 700 T; 0 U; 0 Other;
Query Match 33.0%; Score 875; DB 2; Length 2423;
Best Local Similarity 66.5%; Pred. No. 3e-225;
Matches 1326; Conservative 0; Mismatches 640; Indels 27; Gaps 4;
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QY 206 TCATTATAGTCAAACTGTAGCTTCAATGCTGATTTGGATTTGGTTCTTCGATGATGA 265
DB 291 TGAATGTTTACCACTTCCATTGCTGTTCTTATTTGGTTGCACTGTTATGCTCGTTGGAGGA 350
QY 266 ANTCTTGGTCTTCTCAATCAAAAACCTATTGAACCTTATTAACCAATAATTGATAAGAAG 325
DB 351 GATCCGGTTCTGGGAATTCAAAACGTCGAGCCCTTTAAGCCTTTTGGTTATTAAGCCCTC 410
QY 326 AAGAGAGATTGAAGTTGATCTCTGGTAAATTTAAGCTCACTATATATTTTGGTACTCAGA 385
DB 411 GTGAGGA---AGAGATTGATGATGGCGTAAAGAAATTAACCATCTTTTCGGTACACAAA 467
QY 386 CTGGTACTGCTCAAGGATTTGTAAAGGCATTTGGCAGAGAAATTAAGGCAAAAGTACAAGA 445
DB 468 CTGGTACTGCTGAAGGTTTTCAAAAGGCTTTAGGAGAAGAAAGCTAAAGCAAGATATGAAA 527
QY 446 AAGCAGTTGTTTAAAGTAGTTGACCTGGATGACTATGACGCCGAGGATGATCAATATGAAG 505
DB 528 AGACCAGATTCAAAATCGTTGATTTGGATGATTTACCGGCTGATGATGATGATGAGG 597
QY 506 AGAAATTAAGAGAAAGAGTCTTTTGGTGTTTTTCATGTTAGTACCCACTTATGTTGATGGTGAGC 565
DB 588 AGAATTTGAAGAAAGAGGATGTGGCTTCTTCTTTAGCCACATATGAGATGGTGAGC 647
QY 566 CAACTGACAATGCTGCGAGATTTTACAATGTTTCACTCAGGAACATGAAAGGGGAGAGT 625
DB 648 CTACCGACAATGCAGCGAGATTTCTACAAATGTTTACCAGGGGGAATGACAGAGAGAAAT 707
QY 626 GGCTTCAGCAACTAACTTATGTTGTTTGGTTTGGTTAACCCTCAATACAGGACGATTTCA 685
DB 708 GGCTTAAGAACTTGAAGTATGGAGTGTGGGATTTAGGAAACAGACAATATGAGCATTTTA 767
QY 686 ACAAGATCGCGGTAGATGTGATGAGCAACTCGGTAAACAAGGTGCAAAAGCGCATTTGTC 745
DB 768 ATAAGTTGCCAAAGTTGTAGATGACATTTCTTGTGCAACAAGGTGCACAGCGTCTTGATC 827
QY 746 AAGTGGGCTCGGTGACGATGATCAATGATTTGAAGATGATTTTACTGTTGGCGAGAAAT 805
DB 828 AAGTTGGTCTTGGAGATGATGACCAAGTGTATTTGAAGATGACTTTTACCGCTTGGCGAGAA 887
QY 806 TGTGTGGACTGAATTTGGATCAGTTGCTCAAAAGATGAGGATGCTGCTCTTCAGTGGCTA 865
DB 888 CATTTGGCCCCGAGCTTGTATCAATACTGAGGAAAGAGGGGATACAGCT---GTTGCCA 944
QY 866 CACCGTATATTGCTACTGTTCTCTGAATACAGGGTAGTGAATTCACGAAACTACGGTCGCG 925
DB 945 CACCATACACTGCAGCTGTGTTAGAATACAGAGTTTCTATTCCAGACTCTGAAGATGCCA 1004
QY 926 CTCTGGATGATAAACACATATAATCTGCTAAACGGGATGTTGATTTGATATTTCTCCATC 985
DB 1005 AATTCAATGATATAACATTTGGCAAAATGGGAATGGTTACACTGTGTTTGTGATGCTCAACATC 1064
QY 986 CTTGAGAGACCAATGTTGCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGATAGATCCT 1045
DB 1065 CTTACAAAGCAATGTGCTGTTTAAAGGAGGAGCTTCATCTCCGAGTCTGATGCTTCTT 1124
QY 1046 GTATACATCTGGAGTTTGCACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATG 1105
DB 1125 GTATCCATTTGAAATTTGACATTTGCTGGAAGTGGACTTTACGATGAATACTGGAGATCATG 1184
QY 1106 TTGGTGTATTACTCTGAGAACTCGGATGAATAACTGTGAGGAAGCAGGGAAGCTGTTGGGTC 1165
DB 1185 TTGGTGTACTTTGTGATAACTTTAAGTGAACCTGTAGATGAAGCTCTTAGATTGCTGGATA 1244
QY 1166 AACCCCTGATTTGCTGTTTTCAAATTCACCGGATAAAGAACGGGTCAACCCAGGGAA 1225
DB 1245 TGTACCTGATACTTATTTCTCACTTCAGCTTGAAAAGAAAGCGGCACCAATCAGCA 1304
QY 1226 GTCATTATACCACCTCTCTTTCAGGTCCTTTGACCTTACGATCTGCGCTTAGCACGCTATG 1285
DB 1305 GCTCACTGCTCTCTCTCTCCCA---CCTTGCAACTTGAAGACAGCGCTTACACGATATG 1361
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FT	/transl_except= AGA encodes Lys.	QY	626	GGCTTCAGCAACTAACTTATGTTGGTTTGGTTAAACCGTCAATACGAGCATTTTCA	685
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FT	/*tag= x	Db	521	ACAAGATTGCAATTAGTGGTTGATGAGGGTCTCACAGAGCAGGGTGCACAAAGCGCTTTGTTTC	580
FT	misc_difference 1993. .1995				
FT	/transl_except= CGC encodes Lys.	QY	746	AAAGTGGGCTCGGTGACGATGATCAATGATTTGAAGATGATTTTACTGCTCGCGAGAT	805
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FT	/transl_except= AGA encodes Lys.	Db	581	CAGTTGGCCCTTGGAGATGACGATCAATCAATTGAAGATGATTTTCTGATGGAAGAAT	640
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FT	/transl_except= CGT encodes Lys.	Db	641	TAGTGTGGCTGAATTTGGATCAATTTGCTTCTTGAAGACGACGAAGACTGCT--GCCA	697
PN	W09321326-A2.				
PN	28-OCT-1993.	QY	866	CACCGTATATTGCTACTGTTCTGTAATACAGGGTAGTGTTCACGNAACTACGGTCGGG	925
PD					
PF	13-APR-1993; 93WO-FR000367.	Db	698	CTCCTTACACAGCTGCCATTTCCGAATCCGAGTCTGTTTTCATGACAAACCTGATACGT	757
PR	13-APR-1992; 92FR-00004491.				
PR	(ORSA-) ORSAN.	QY	926	CTCTGATGATAAACACATATAATCTGCTAACCGGATGCTGCAITTTGATATTTCTCCATC	985
XX		Db	758	TTTCCGAGATCATAGTCAAA-----CTAATGGTCACTACTGTTACGATGCTCAACATC	811
XX	Kazmaier M, Iacroute F, Mignotte-Vieux C, Minet M, Pompon D;	QY	986	CTTGCAGAACCAATTTGTTGCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGTAGATCCT	1045
XX	WPI; 1993-351736/44.	Db	812	CATGCAGATCCAAACGTGGCTGTTAAAAAAGAGCTCCATACCCCTGAATCCGATCGCTCT	871
DR	P-PSDB; AAR43583.				
XX	New DNA encoding plant NADPH cytochrome P450 reductase - cloned by	QY	1046	GTATACATCTGAGTTGACATATCAGGCTCTTCCCTTACATATGATGAGCTGAGATCATG	1105
PT	functional complementation in yeast, also recombinant enzyme useful in	Db	872	GCACTCATCTTGAATTTGACATCTCTCACACTGGACTATCATACGAAATCTGGGATCACG	931
PT	P450 mediated bioconversion processes.				
XX	Claim 11; Fig 11; 79pp; French.	QY	1106	TTGGTGTTTATGCTGAGAACTCGGATGAACTGTCGAGGAACGAGGAAGCTGTTGGGTC	1165
PS		Db	932	TCGGTGTCTACTGTGAACCTTAATTTGAAGTAGTGGAGGAAGCTGAGAACTGTATAGGAT	991
XX	A new method for determining whether a DNA sequence encodes an NADPH	QY	1166	AACCCCTCGAATTTGCTGTTTCAATTCACCGATTAAGAAGACGGGTCAACCCAGGGAA	1225
CC	cytochrome P450 reductase involves transforming yeasts with plasmids of a	Db	992	TACCAGCAGATACTATTCTTCTATTACATTTGATTAACGAAGATGGAACACCACCTCGGTG	1051
CC	total cDNA bank of plant(s). The yeasts used in the procedure are	QY	1226	GCTCATTTACCCTCGTTTCCAGGTCCTTGACCTTAGCATCTGCCCTAGCACGCTATG	1285
CC	incapable of producing their own NADPH cytochrome P450 reductase. They	Db	1052	GACCTACATGTCAGGCTCTCTTCCCTCCCTGCACTTTAAGAAAAGCAATGACCAATTACG	1111
CC	are then exposed to a cytochrome P450 inhibitor at a level which is	QY	1286	CTGATCTTTTGAATCTCTCTAGAAAGGCTTCTCTGATTCCTCTGTCGCTCATGATCTG	1345
CC	lethal to the yeast cells but not to cells which, because of the	Db	1112	CAGATCTGTTGAGTTCTCCAAAAGTCAACCTTGTCTGCTAGCTGCGCATGCTTCTG	1171
CC	transformation, now contain an active NADPH cytochrome P450 reductase.	QY	1346	TACCCAGTGAACGACAGAGATTTGCGCTTTTGTCTACCTCTGGGAAAGAATGAGTATT	1405
CC	Surviving clones are then isolated and plasmid DNA extracted. The gene is	Db	1172	ATGCCACTGAAGCTGATCGACTACAATTTCTTGTGCTCTCGTGAGGCAAGGATGAATATG	1231
CC	inserted into the plasmid at a site which places it under the control of	QY	1406	CAAAATGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGGCCGAGTTTCCATCAG	1465
CC	an inducible promoter. (Updated on 25-MAR-2003 to correct PN field.)	Db	1232	CTGAATGGATTGTTGCAAAACCAAGAAGCTTCTTTGAGGTCAATGAAGCTTTTTCGCTAG	1291
CC	(Updated on 27-AUG-2003 to correct OS field.)	QY	1466	CAAAACCCCTCTGCTGTTGTTCTTTGCTGAGTAGCCCTCGCTTACCGCCTCGATACT	1525
XX	Sequence 2112 BP; 591 A; 422 C; 506 G; 593 T; 0 U; 0 Other;	Db	1292	CTAAACCTCGCTCGGGTCTTTCTTTGAGCTATTGGCCCGGTTTGCAGCCTCGATACT	1351
Query Match	32.5%; Score 859.8; DB 2; Length 2112;	QY	1526	ATTCTATCTCATCTCTCTCTAAAGTTTGTCTCCTCAAGAAATTCATGTGACGTGTGCTTTAG	1585
Best Local Similarity	67.6%; Pred. No. 3.6e-221;	Db	1352	ACTCTATTTCTCTCTCCCAAGATGGTACCACCAAGAGATTCTATGTTAGCTGTGCATTAG	1411
Matches 1263; Conservative	0; Mismatches 582; Indels 24; Gaps 3;	QY	1586	TATATGGTCAAGCCCTACCGGAAGGGTTTCCAGGAGGTGTTCGACATCGATGAAGC	1645
QY	326 AAGAGAGATTGAAGTTGATCTCGGTGTAATAAATTAAAGTCACTATATTTTGGTACTCAGA	Db	1412	TTTATGAGAAGACTCTCTGGAGGTCGTATCCAAAAGGAATATGCTCAACCTCGATGAAGA	1471
Db	161 AGGTGAGCAGGAGGTTGATGACGGTAAAGAAGGTTACGATATTTTTCGGAACGCAAA	QY	1646	ATGCAAGTTCTCT-----CAGGATAGCTGGGCTCTATTTTGTTCGAACGT	1690
QY	386 CTGGTACTCTGAAGGATTTGCTTAAGGCATTGCGAAGAAATTAAGGCAAGTACAAGA	Db	1472	ATGCTGTGCTTTGACCGGAATCAAGATTGAGCTCGGCCCATTTTGTGTAACAT	1531
Db	221 CTGGAACCGCTGAGGTTTGTCTAAGCGCTGTTTGAAGAAGCGAAGCGCGATATGA	QY			
QY	446 AAGCAGTTGTTAAAGTAGTTGACCTCGATGACTATGACGCGAGGATGATCAATATGAAG	Db			
Db	281 AAGCTGTGTTAAAGTGGTTGATTGGATGATTAATGCTGCTGATGATGAGGATGTCAG	QY			
QY	506 AGAAATTAAGAAAGAGTCTTGGTGTTCATGTTAGTACGCCATTAATGTTGATGTTGAGC	Db			
Db	341 AGAAATTCAGAGGAGAGACATTTGCTTTCTTCTTCTTGGCTACATATGAGATGGTGAGC	QY			
QY	566 CAACTGACATGCTCGAGATTTTACAATGTTTCACTCAGGAACATGAAGGGGAGCT	Db			

ammonia lyase (TAL) activity from the yeast *Rhodotorula glutinis* plus the plant cytochrome p-450 and the cytochrome p-450 reductase into *E. coli*. Nucleic acid encoding mutant TAL enzyme is useful for producing PHCA by recombinant techniques. The recombinantly produced PHCA may be used as a monomer for production of liquid crystal polymers (LCP). LCP may be used in electronic connectors and telecommunication and aerospace applications. LCP resistance to sterilising radiation has also enabled these materials to be used in medical devices as well as chemical, and food packaging applications. The present sequence is *Helianthus tuberosus* cytochrome p-450 reductase DNA

SQ Sequence 1863 BP; 531 A; 382 C; 424 G; 526 T; 0 U; 0 Other;

Query Match

Query Match
Best Local Similarity 30.3%; SCORE 807.6; DB 6; Length 1863;
Best Local Similarity 67.2%; Pred. No. 4.2e-207;

Desc Local Similarity 87.2%; Fied. NO: 4.2E-207;
Matches 1197: Conservative 0: Mismatches 559: Indels 24: Gaps 3:

415	QY	TTGGCAGAGAAATTAAAGGCAAAAGTACAAGAAACAGTTGTTAAAGTAGTTGACCTGGAT	474
1	DB	TTGTTTGAAGAAGCGAAAGCGCGATCAAAAAGCTGTGTTTAAAGTGGTTGATTTGGAT	60
475	QY	GACTATCAGCCGAGGATGATCAATATGAAGAGAAATTAAGAAGAGTCTTTGGTGTCTT	534
61	DB	GATTATGCTGCTGATGATGAGGAGTATGCAGAGAAATTCAGAAGGAGACATTTGCTTTTC	120
535	QY	TTCAATGTTAGCCATTATGTTGATGTTGAGCCAACTGACAAATGCTCGGAGATTTTACAAA	594
121	DB	TTCTTCTTGGCTACATATGGAGATGGTGAGCCAACTGATAATGCTGCAAGATTTTATAAA	180
595	QY	TGTTTCACTCAGGNACATGAAGGGGAGAGTGGCTTCAGCAACTAACTTATGGTGTCTTT	654
181	DB	TGGTTTCAACCGGAGAGATGAAGAAGAGTTTGGCTTCAAAACCTTCACTATGGTGTCTTT	240
655	QY	GGTTTGGGTAAACCGTCAATACGAGCATTTCAAACAAGATCGCGGTAGATGTGGATGAGCAA	714
241	DB	GGCTTTGGCAACAAACAGTATGACATTTCAAACAGATTGCATTAGTTGGTTGATGAGGGT	300
715	QY	CTCGGTAAACAAGTGCAAAGCGCATTTGTTCAAAGTGGGGTCCGGTAGCAGTATCAATGC	774
301	DB	CTCACAGAGCAGGGTGCAAAAGCGCTTTGTTCCAGTTGGCCTTGAGATGACGATCAATCA	360
775	QY	ATTGAAGATCATTTTACTGCTTCGCGAGAAATTTGTGTGGACTGAATTTGGATCAGTTGCTC	834
361	DB	ATTGAAGATGATTTTTCTCGATGAAAGAATTAGTGTGGCCTGAAATTTGGATCAATTTGCTT	420
835	QY	AAAGATGAGGATGCTGCTCTTCAGTGGCTACACCGTATATTGCTACTGTTTCTCGTAATAC	894
421	DB	CTTTGATGAAGACGACAAAGACT--GCTGCGCACTCCTTTACACAGCTGCCATTCGCGAATAC	477
895	QY	AGGGTAGTGATTCACGNAACCTACGGTCGGGCTCTGGATGATAAACATATAATCTGCT	954
478	DB	CGAGTCGTGTGTTTATGACAAACCTGATACGTTTTCGAGAATCA-----TAGTCAAACCT	531
955	QY	AACGGCGATGTTGCATTTTGATATTCTCCATCCTTGCAGAACCAATTTGTGCTCAACAAGA	1014
532	DB	AATGGTCATACTGTTACGATGCTCAACATCCATCGAGATCCAACTGGGCTGTATAAAA	591
1015	QY	GAGCTCCAACAAACCCAGTCTGATAGATCCCTGTATACATCTGGAGTTTCGATATCAGGC	1074
592	DB	GAGCTCCATACCCCTGAAATCCGATCGCTCTCGCACTCATCTTGAAATTTGCATCTCTCAC	651
1075	QY	TCFTTCCCTTACATATGAGACTCGAGATCATGTTGGTGTGTTTATGCTGAGACTCGGATGA	1134
652	DB	ACTGGACTATCATCGAACTGGGATTCAGTCGGTGTCTACTGTGAAAAACCTTAATTGAA	711
1135	QY	ACTGTCGAGGAACGGGAAGCTGTTGGGTCAACCCCTGGATTGCTGTTTTCCTCAATTTCAC	1194
712	DB	GTAGTGGAGAACTCGAGAACTGATAGGATTTACCAGCAGATACTTATTCTCATTTACAC	771
1195	QY	ACGGATTAAGAACACGGGTCAACCCAGGGAAGCTCATTAACCACTGCTTCTCCAGGTCCT	1254
772	DB	ATTGATTAACGAAGATGGAACACCACTCGGTGGACCTTACATTTGAGCGCTCTCTTCCCTCCC	831

DE	Helianthus tuberosus cytochrome P-450 reductase enzyme DNA.
XX	
XX	Phenylalanine ammonia-lyase; PAL; enzyme; cinamate; food packing; PHCA;
KW	para-hydroxycinnamic acid; tyrosine ammonia-lyase; TAL; medical device;
KW	Liquid Crystal Polymer; LCP; electronic connector; Jerusalem artichoke;
KW	aerospace application; cytochrome P-450 reductase; telecommunication;
KW	chemical; ds.
XX	
OS	Helianthus tuberosus.
XX	
Key	Location/Qualifiers
FT	1..1767
CDS	*tag= a
FT	/product= "H. tuberosus cytochrome P-450 reductase"
FT	/note= "CDS does not include start codon"
FT	/partial
XX	
WO	200111071-A2.
PX	
PN	
PD	15-FEB-2001.
XX	
PF	03-AUG-2000; 2000WO-US021156.
PP	
XX	
PR	06-AUG-1999; 99US-0147719P.
XX	
PA	(DUPO) DU PONT DE NEWMOURS & CO E I.
PI	Tang X, Vannelli TM, Qi WM, Sariaslani S, Gatenby AA;
XX	
WP	I; 2002-121549/16.
DR	P-PSDB; AAB16392.
XX	
PT	Producing para-hydroxycinnamic acid for producing liquid crystal polymer,
PT	comprises converting cinnamate to PHCA, glucose to PHCA by phenyl ammonia
PT	-lyase route, or generating a biocatalyst with tyrosine ammonia-lyase
PT	activity.
XX	
PS	Claim 20; Page 73; 75pp; English.
XX	
CC	The invention relates to a method for producing para-hydroxycinnamic acid
CC	(PHCA). The method comprises converting cinnamate to PHCA by converting
CC	glucose to phenylalanine to PHCA through the phenyl ammonia-lyase (PAL)
CC	route or by generating a new biocatalyst possessing enhanced tyrosine
CC	ammonia-lyase (TAL) activity. The method is useful for the biological
CC	production of PHCA which is useful as a monomer for the production of
CC	Liquid Crystal Polymers (LCP), where the LCP is used in electronic
CC	connectors, telecommunications and aerospace applications. LCP is also
CC	useful in medical devices, as well as chemical, and food packing
CC	applications due to its resistance to sterilising radiation. The present
CC	sequence is Jerusalem artichoke (Helianthus tuberosus) cytochrome P-450
CC	reductase enzyme DNA. Cytochrome P-450 and cytochrome P-450 reductase are
CC	useful for the conversion of cinnamate to PHCA
XX	
SQ	Sequence 1863 BP; 531 A; 382 C; 424 G; 526 T; 0 U; 0 Other;
	Query Match 30.5%; Score 807.6; DB 6; Length 1863;
	Best Local Similarity 67.2%; Pred. No. 4.2e-207;
	Matches 1197; Conservative 0; Mismatches 559; Indels 24; Gaps 3;
QY	415 TTGGCAGAGAATTAAGGCAAGGTACAGAAAGCAGTTGTAAAGTAGTTTGACTCGAT 474
Dd	1 TTGTTTGAAGAACGMAAGCGCATATGAAGAGCTGTGTTTAAAGTGTTGATTGGAT 60
QY	475 GACTATGCAGCCGAGGATGATCAATATGAAGAGAAAATTAAGAAAGAGTCTTTGGTGT 534
Dd	61 GATTATGCTGTGATGATGAGGAGTATGCAGAGAAATTAAGAAAGGACATTTGCTTC 120
QY	535 TTCATGGTAGCACCTTATGGTATGGTGTGAGCCAACTGACATGCTGCCAGATTTTACAA 594
Dd	121 TTCTTCTTGGCTACATATGAGATGGTGTGAGCCAACTGATAATGCTGCAAGATTTTATAA 180
QY	595 TGCTTCACTCAGGAAACATGAAAGGGGAGAGTGGCTTCAGCAACTAACTTATGTGTGTTT 654

QY 1720 ACTCAATTATCATGTTGGACCTGGTACAGGGTTAGCTCTTTTCAGAGGATTTCTGCAG 1779
 DB |||||
 QY 1312 GTCCCGGTATCATGATTTGCCCTTGGAAACGGGTGCTGCTGTTAGAGGTTTCTTCAA 1371
 DB |||||
 QY 1780 GAAAGAAATGCGCCCTCAAGGAAATGTTGCTCAACTTGGCCCGACAGTGTCTTTTTCGGA 1839
 DB |||||
 QY 1372 GAAAGATTAGCTCTCAAGGAATCTGGAACCGAACTCGGTCAATCCATTTTGTCTTCGGT 1431
 DB |||||
 QY 1840 TGTAGGAATCGTAATATGGACTTTCATTTATGAGACCAACTAACCACTTCGTGGAACGA 1899
 DB |||||
 QY 1432 TGCAGAAACCGTAAGTGGATTTTCATATATGAGAACTGAACCAACTTTGTGAAAT 1491
 DB |||||
 QY 1900 GGAATCTCAATTCGGAGCTAGTTATTGCTCTTTTTCAGCTGAAGGGAAGAAAGGAATATGTT 1959
 DB |||||
 QY 1492 GCGCGCTTTCCGAGCTTGACATGGCTTTCTTCGGAAGGCGCATCTAAGATATAGTG 1551
 DB |||||
 QY 1960 CAACATAAGATGATGGAAGAACCGATGTATGGAATGTGATATCAGGGGACGGTTAT 2019
 DB |||||
 QY 1552 CAACATAAATGAGCCAAAGGCTTCGATATATGGAACATGCTTTCTGAGGGAGCATAC 1611
 DB |||||
 QY 2020 CTCTATGTGTGTTGATGATCCAGGGAATGCCAGAGATGTCATCCACGTTGCATACC 2079
 DB |||||
 QY 1612 TTATACGTGTGTGATGCAAGGCTGCTTAAAGATGTACACCGAACCTTTCACACC 1671
 DB |||||
 QY 2080 ATTGCCCAAGAACAGGACCCATGGAATCATCTGCTGCCGAAGCTGCAGTAAAGAACTC 2139
 DB |||||
 QY 1672 ATTGTGCAAGAACAGGGAATTTGGATTCCTCTTAAGCAGAGCTGTATGTGAAGATCTA 1731
 DB |||||
 QY 2140 CAAGTTGAAGAACGATATCTAAGAGATGTCTGTGATCGA 2179
 DB |||||
 QY 1732 CAAATGTCGGAAGATACCTCCGTGATGTTTGTGTGATCTA 1771
 DB |||||

RESULT 12

ADJ10845
 ID ADJ10845 standard; DNA; 1985 BP.
 XX
 AC ADJ10845;
 XX
 AC ADJ10845;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Recombinant tomato DNA to generate disease resistant plants SeqID 241.
 XX
 KW genetically engineered; plant; Avr-Pto; avirulent Pto;
 KW bacterial speck disease; tomato; transgenic; biotic; abiotic stress; ds;
 KW Pfi.
 XX
 OS Lycopersicon esculentum.
 XX
 XX US2004006787-A1.
 XX
 XX 08-JAN-2004.
 XX
 XX 14-JAN-2003; 2003US-00341961.
 XX
 XX 14-JAN-2002; 2002US-0348792P.
 PR
 PR 20-JUN-2002; 2002US-0390249P.
 XX
 XX (MART/) MARTIN G B.
 PA (MYSO/) MYSORE K K.
 PA (CRAS/) CRASTA O R.
 PA (FOLK/) FOLKERTS O.
 PA (SWIR/) SWIRSKY P.
 XX
 XX Martin GB, Mysore KK, Crastra OR, Folkerts O, Swirsky P;
 PI WPI; 2004-081759/08.
 XX
 XX New genetically engineered plant comprising a recombinant polynucleotide
 PT showing expression associated with Avr-Pto mediated defense response,
 PT useful in increasing resistance of plant against bacterial speck disease.
 XX

PS Claim 5; SEQ ID NO 241; 176pp; English.

XX This invention relates to a method of generating novel genetically
 CC engineered plants. Specifically, it refers to compositions useful for
 CC transforming plants with a recombinant polynucleotide or plant gene that
 CC shows a specific pattern of expression associated with the Avr-Pto
 CC mediated defense response. Avr-Pto is described as the avirulent Pto gene
 CC found in *Pseudomonas syringae* pathovar tomato strain [strain T1(A)],
 CC which mediates bacterial speck disease in tomato plants. The present
 CC invention describes identifying genes that are up- or down- regulated in
 CC the defense response and that are involved in the interaction of Avr-Pto
 CC with Pto and/ or Pfi. As such, these novel recombinant polynucleotides
 CC can be used to generate transgenic plants that are resistant to bacterial
 CC speck disease and furthermore exhibit increased resistance against biotic
 CC and abiotic stresses. This polynucleotide sequence is a recombinant
 CC tomato polynucleotide used to generate genetically engineered, disease
 CC resistant plants of the invention.

XX SQ Sequence 1985 BP; 538 A; 379 C; 464 G; 604 T; 0 U; 0 Other;

Query Match 29.1%; Score 770.2; DB 12; Length 1985;
 Best Local Similarity 68.0%; Pred. No. 5.5e-197;
 Matches 1126; Conservative 0; Mismatches 508; Indels 21; Gaps 3;

QY 542 TAGCCACTTATGTGTGATGGTGAGCCAACTGACAACTGCGAGATTTTACAAATGGTTCA 601
 DB |||||
 QY 3 TGGCAACATATGGAGATGGTGAACCACTGATANTCTGCCAGATTTCTATAATGGTTTG 62
 DB |||||
 QY 602 CTCAGGAACATGAAGGGGAGAGTGGCTTTCAGCAACTTAATATGTTGTTTGGTTGG 661
 DB |||||
 QY 63 AAGAGGGGAAAGAGAGGGGTGACTGCTTTAAGAACTCTTCAGTATGAGTATTTGGGCTTG 122
 DB |||||
 QY 662 GTAACCGTCAATACGAGCATTTCAACAAGATCCGGTAGATGGGATGAGCACTCGGTA 721
 DB |||||
 QY 123 GCAACAGACAATACGAGCATTTTAAACAGATGTCTAAAGTTGTCGATGAGCTTCTGGCTG 182
 QY 722 AACAAAGTGCAGAAAGCGCATTTGTTCAAGTGGGGCTCGGTGACGATGATCAATGCAATTGAAG 781
 DB |||||
 QY 183 AGCAAGTGGGAGAGGCTTTGTTCCAGTGGGTCTTGGAGATGATGATCAATGCAATTGAAG 242
 QY 782 ATGATTTTACTGCTTGGCGAGAAATTTGTTGGACTGAAATGGATCAGTTGCTCAAGATG 841
 DB |||||
 QY 243 ATGATTTTCTGTCATGGCGTGTAGTGTGCGCTGAAATAGATAAGTTGCTTCTTGACG 302
 QY 842 AGGATCTCTCTCTTCAGTGGCTACACCGTATATTTGCTACTGTTCTGATACAGGGTAG 901
 DB |||||
 QY 303 GGGATGATGCAACT---GCTACAACCTCCATATACCTGCTGCTGTTTGGAAATATAGGGTTG 359
 QY 902 TGATTCACGAAACTACGGTCCGGGCTCTGGATGATAAACAACATAAA---TACTGCTAAACG 958
 DB |||||
 QY 360 TTACCTATGCAAGTCCAACTTTTGATACGACTTGGACCAACCAATGTCATGCAAAATG 419
 QY 959 GCGATGTTGCATTTGATATTTCTCCATCTCTTGGAGAACCAATGTTGCTCAACAAAGAGAGC 1018
 DB |||||
 QY 420 GACATGTCATCGTTGATGCTCAACATCTCTGTCAGAGCTAATGTTGCTGTGAGGAAGAGC 479
 QY 1019 TCCAGAAACCCAGTCTGATAGATCTCTGTATACATCTGAGTTCGACATATCAGGCTCTT 1078
 DB |||||
 QY 480 TTCATACCTCCAGCTTCTGATCGTCTTTCGACATCATCTGGAGTTGACATTTCTTGCACGTG 539
 QY 1079 CCCTTACATATGAGACTGGAGATCATGTTGGTGTGTTTATGCTGAGAACTGCGATGAAACTG 1138
 DB |||||
 QY 540 GACTTACGTACGAACTGGTGTATCATGTTGGTGTGTGTAATGTAATTTTGTGAAACCG 599
 QY 1139 TCGAGGAACGAGGAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTCAATTTCAACCG 1198
 DB |||||
 QY 600 TGGAGGAAGCTGAAAGGCTACTGAAATATATCACCGGATACTTTCTTTTCCATTCACACCG 659
 QY 1199 ATAAAGAACCGGTCACCCGAGGAGCTCAATTACCACTCTTTCAGGCTCTTTCGCA 1258
 DB |||||
 QY 660 ATAAAGAGATGGCACACCACTTGGTGGAAAGTTCAATTCGCATCTCCATCTCCCTCTTGA 719
 QY 1259 CTTTACGATCTGCCCTAGCACGCTGATGCTCTTTTGAATCCTCTCTAGAAAGGCTTCTC 1318

Db	720	CTTTGGAAACAGCAATTGACTCGGTATGCTGATGTTTGGTTCCTCTAAAGAGCTCTCTT	779
Qy	1319	TGATTGCTGTGTCGGCTCATGTCATCCCAAGTGAAGCAGAGAGATTCGGCTTTTGT	1378
Db	780	TACTTGTCTTAGCGGCATGTTCTTCTGATCCAAATGAAGCTGATCGATTAAGATATCTAG	839
Qy	1379	CATCACCTCTGGGGAAGAATAGATTTCAAAAATGGGTAGTTGGAAATCAGAGAGTCTTT	1438
Db	840	CATCACCTCTGGAAAGAAAGATATGCTCAGTGGATAGTTGCAAGTCAGAGAAGCCTTC	899
Qy	1439	TGAGATCATGCGCCAGGTTTCCATCAGCAAAACCCCTCTTGTGTGTTCTTTGCTGCAG	1498
Db	900	TTGAATCATGGCTGAATTTCTTCAGCCAAAGCCTTCAATCGGTGTTTTCTTTGCTTCG	959
Qy	1499	TAGCCCTCTGCTTACCGCCTCGATCTATTCTATCTCATCTCTCTCTAAAGTTTGCCTCC	1558
Db	960	TTGCTCTCGCTACAAACCAAGATTTCTACTCCATCTCATCATCTCTAGGATCGCGCAT	1019
Qy	1559	CAAGAAATCATGTGACGTGTGCTTTAGTATATGGTCAAAGCCCTACCGGAAGGTTCAAC	1618
Db	1020	CTAGAATTCATGTCACTTTGTGCACTGGTTTACGACAAAATGCCAACTGGACGAATTCAC	1079
Qy	1619	GAGGAGTGTCTTGGACATGGATGAAGCATGCAGTTCCTCAGGA-----TA	1663
Db	1080	AGGTTGTCCTCAACATGATGAAGAAATGCTATTCTCTAGAAGAAAGCCTTTCCTGCA	1139
Qy	1664	GCTGGGCTCTATTTTGTGTCGAAGTCAAACTTCAAGTTTACAGCTGACCCCTCAACTC	1723
Db	1140	GTACGGCACCTATTTTGTTCGGCAATCAAACTTTTAAACTGCCAGCTGATAACAAGTTC	1199
Qy	1724	CAATTATCATGTTGGGACCTGGTACAGGTTAGCTCTCTTTCAGAGGATTTCTCGAGAA	1783
Db	1200	CAATCATATGATTTGGCCCTGGTACTGGATTGGACCAATTCAGGGGTTTTCTCCAGAAA	1259
Qy	1784	GAATGGCCCTCAAAGGAAATGTTGCTCAACTTGGCCACAGCTGCTCTTTTCGGATGTA	1843
Db	1260	GAATGGCTTTGAAGGAGGAGGAGCTGACCTTGGTCTGTCAGTGTATTTTGGATGCA	1319
Qy	1844	GGAAATCGTATATGGACTTCATTATTAAGACGAACTAAACAACCTTCGTGGAAACGAGGAG	1903
Db	1320	GSAAACGCCAAATGGACTACATCTATCAGGATGAGTTAGATAACTTCTTGAAGCCGGTG	1379
Qy	1904	TCAATTCGGAGCTAGTTATTTGCTTTTTCAGTGAAGGGGAAAGAGGAATATGTTCAAC	1963
Db	1380	CACCTTCTAATCTAGTTGTGGCTTCTCAGCTGAAGGACCTAACAAAGAATATGTGCAC	1439
Qy	1964	ATAAGATGATGGAGAAACCAACGGATGTATGGAAATGTGATATCAGGGGACGGTTATCTCT	2023
Db	1440	ATAAAATGACACAGAAGCGGACACATCTGGAACATGATTTCTCAGGGGAGGTTATGTTT	1499
Qy	2024	ATGTGTGTGGTATGCCAAGGGAAATGGCCAGAGATGTCCATCGCATCGTTGCATACCATTG	2083
Db	1500	ATGTGTGTGTGATGTCTAAGGGCATGCCAGGAGATGTCCATCGGAACCTTTCACACTATTG	1559
Qy	2084	CCCAAGAACAGGGACCCCATCGAATCATCTGCTGCCGAAGCTGCAGTAAAGAAACTCCAAG	2143
Db	1560	CTCAGGATCAGGGATCACTTGTATAGTCTTCAAGCCGAGACCTTTGTCAAGAAATTCGAA	1619
Qy	2144	TTGAAGAACGATATCTAAGAGATGTCTGTGTATCG	2178
Db	1620	CGACCGGAAGATATCTGCGTGAATGTTGGTAAATTG	1654

RESULT 13

ADA70621

ID ADA70621 standard; DNA; 2016 BP.

XX
AC

XX
DT 20-NOV-70

DT 20-NOV-2003 (first entry)

XX DE Rice gene, SEQ ID 3944.

XX Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
XX
OS *Oryza sativa*.
XX WO2003000898-A1.
XX
XX 03-JAN-2003.
XX
XX 22-JUN-2001; 2001WO-IB001105.
XX
XX 22-JUN-2001; 2001WO-IB001105.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX
XX Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
XX Claim 6; SEQ ID NO 3944; 899pp; English.
XX
XX The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
XX Sequence 2016 BP; 484 A; 464 C; 576 G; 487 T; 0 U; 5 Other;

RESULT 13

ADA70621

ID ADA70621 standard; DNA; 2016 BP.

XX
AC

[illegible]

DT 20-NOV-2003 (first entry)

XX DE Rice gene, SEQ ID 3944.

Qy	739	ATTGTTCAAGTGGGGCTCGGTGACGATGATCAATGCAATTGAAGATGATTTTACTGCTTGG	798
Db	691	ATTGTTCCCTCTTGCTTTGGAGATGATGATCAATGCAATTGAAGATGACTTTCAATGCAATGG	750
Qy	799	CGAGAAATGTTGTGGACATGGAATTCGATCAGTTGCTCAAGATGAGGATGCTGCTCCTTCA	858
Db	751	AAGGAACTTCTATGGCCAGAATTGGATTAATTTGCTCCGTGTTGAAGATGATAAATCGGCA	810
Qy	859	GTGGCTACACCGTATATTGCTACTGTTTCTCGAATACAGGGTAGTGATTCACGAAACTACG	918
Db	811	GCACCAACTCCCTACACAGCTGCTATTCTCTGAAATATAGAGTTGATTTGGTCAAGCCAGAG	870
Qy	919	GTCCGGGCTGTGGATGATAAACACATAAATACTGCTTAACGGCGAGTTGGATTTGATATT	978
Db	871	GAAGCCATGCAATATCAACAAATCCCTTTAGTCTCAGTAATGGTCAATGCTGCTATATGACATT	930
Qy	979	CTCCATCCTTCAGAAACCATTTGCTCAACAAAGAGAGCTCCACAAACCCAGTCTGAT	1038
Db	931	CAGCATCCTTCAGAGCAAAATGTGGCTGTGGCGGGAGCTTTCACAGCCGGCTTCTTAC	990
Qy	1039	AGATCTCTGTATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACATATGAGACTGGA	1098
Db	991	CGGTCTGCAATTTAGAGTTTGATATTTACGGGACTGGTCTTACATATGAGACTGGA	1050
Qy	1099	GATCATGTTGGTGTATTGCTGAGAACTGGGATGAATCTGTGAGGA-AGCAGGGGAAGCT	1157
Db	1051	GATCATGTTGGTGTATATGCAGAAAACTGCACAGAGACTGTGAGAGGAGAGTGTCTTTAATT	1110
Qy	1158	GTTGGGTCAACCCCTGGATTTGCTGTTTCAATTCACACGGATTAAGAAAGACGGGTCAAC	1217
Db	1111	GCITTTGGCTTCCCATGCACTGATCCCAAAGATGCTCAGAGGGCTAAGA-----	1158
Qy	1218	CCAGGAAAGCTCATTAACACCTCTTTCCAGGTCTTTCACCTTACGATCTGCGCTAGC	1277
Db	1159	-----	1158
Qy	1278	ACGCTATGCTGATCTTTTGAATCCTCTAGAAAGGCTTCTCTGATGCTCTGTCGCTCA	1337
Db	1159	-----CATCTAGCATCTCTGCTGGAAAGTTTGTGCTTCA	1195
Qy	1338	TGCATCTGTACCCAGTGAAGCAGAGAGATTGGCGCTTTTGTGATCATCCTCTGGAAGAA	1397
Db	1196	TGAGCTTCA-----TTTGGCAGAA	1214
Qy	1398	TGAGTATTCAAAATGGGTAGTTGGAAGTCAAGAGAGTCTTTTGGAGATCATGTCGCCAGTT	1457
Db	1215	GGAGTATTCTCAATGGATAGTTTCAAGTCAACGGAGTCTCTTGGAGTTATGACAGATT	1274
Qy	1458	TCCATCAGCAAAACCCCTCTGGTGTGTTCTTTGCTGCAAGTACGCCCTCGCTTACCGCC	1517
Db	1275	CCCATCAGCAAAAGCCTCAACTTGGTGTCTTCTTTGCAGCCATTGCTCTCGATGCGAGCC	1334
Qy	1518	TCGATACTATTCTATCTCATCC-----TCTCCTTAAGTTTGCTTCCCTCAAGAATTCA	1568
Db	1335	GAGATACTACTCGATATCTCCCTTAACCGAGTKMCCCTTGGATGACTCCCAACAAGAATTCA	1394
Qy	1569	TGTGACGTGTGCTTTTACTATATGTTCAAGCCCTTACCGGAAGGTTTCAACCGAGAGTGTG	1628
Db	1395	TGTAAATGTGCGCTAGTGTATGGCAAAACCCCTTACTGGAAGGATCCATAAAGAGTTTG	1454
Qy	1629	TTCGACATGGATGAAGCATGCAGTTCCCTCAGGA-----TAGCTGGGCTCC	1673
Db	1455	TTCTACTTGGATGAAGAACTCGATTCTCTTTGGAAGAGAGCCAAAGATTGATGCTGGGCTCC	1514
Qy	1674	TATTTTGTTCGAACGTCAAACTTCAAGTTTACAGCTGACCCCTCAACTCCCAATTATCAT	1733
Db	1515	AAATTTTGTTAGCGAGTCAAACTTCAAACTGCGCTACTGATCTTACTGTGCTTATTATAAT	1574
Qy	1734	GGTGGGACCTGGTACAGGGTTAGTCTCTTTTCAGAGGATTTTCTCAGGAAGATGSCCCT	1793
Db	1575	GATAGTCTCGAACTGGTCTTGCACTTTTAGGGCTTCTTACAGAAAGATTAGCTCT	1634
Qy	1794	CAAGGAAATGGTGTCTCAACTTGGCCACAGCTGCTCTTTTTCGGATGTAGGAATCGTAA	1853

RESULT 14

ADR60759

ID ADR60759 standard; cDNA; 683 BP.

XX

AC ADR60759;
VV

XX
DT 02-DEC-2004 (first entry)

DI 02-DEC-2004 (LIBL ENCLY) XX

DE Cotton cDNA sequence, SEQ ID 1540.

[illegible]

KW Cotton; ss; plant; cold tolerance; growth rate; cell cycle pat.

KW drought tolerance; plant disease resistance; galactomannan; lignin;

plant growth regula

KW homologous recombination
KW pathogen resistance

KW stress resistant
KW pathogen resistant

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OS *Gossypium hirsutum*.

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PN US2004181830-A1.
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PD
16-SEP-2004FD
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16-SEP-2004.

29-JAN-2004; 2004

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PR 07-MAY-2001; 2001US-

PR 12-DEC-2001; 2001US-

2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025 2026 2027 2028 2029 2030 2031 2032 2033 2034 2035 2036 2037 2038 2039 2040 2041 2042 2043 2044 2045 2046 2047 2048 2049 2050 2051 2052 2053 2054 2055 2056 2057 2058 2059 2060 2061 2062 2063 2064 2065 2066 2067 2068 2069 2070 2071 2072 2073 2074 2075 2076 2077 2078 2079 2080 2081 2082 2083 2084 2085 2086 2087 2088 2089 2090 2091 2092 2093 2094 2095 2096 2097 2098 2099 2100 2101 2102 2103 2104 2105 2106 2107 2108 2109 2110 2111 2112 2113 2114 2115 2116 2117 2118 2119 2120 2121 2122 2123 2124 2125 2126 2127 2128 2129 2130 2131 2132 2133 2134 2135 2136 2137 2138 2139 2140 2141 2142 2143 2144 2145 2146 2147 2148 2149 2150 2151 2152 2153 2154 2155 2156 2157 2158 2159 2160 2161 2162 2163 2164 2165 2166 2167 2168 2169 2170 2171 2172 2173 2174 2175 2176 2177 2178 2179 2180 2181 2182 2183 2184 2185 2186 2187 2188 2189 2190 2191 2192 2193 2194 2195 2196 2197 2198 2199 2200 2201 2202 2203 2204 2205 2206 2207 2208 2209 2210 2211 2212 2213 2214 2215 2216 2217 2218 2219 2220 2221 2222 2223 2224 2225 2226 2227 2228 2229 2230 2231 2232 2233 2234 2235 2236 2237 2238 2239 2240 2241 2242 2243 2244 2245 2246 2247 2248 2249 2250 2251 2252 2253 2254 2255 2256 2257 2258 2259 2260 2261 2262 2263 2264 2265 2266 2267 2268 2269 2270 2271 2272 2273 2274 2275 2276 2277 2278 2279 2280 2281 2282 2283 2284 2285 2286 2287 2288 2289 2290 2291 2292 2293 2294 2295 2296 2297 2298 2299 2300 2301 2302 2303 2304 2305 2306 2307 2308 2309 2310 2311 2312 2313 2314 2315 2316 2317 2318 2319 2320 2321 2322 2323 2324 2325 2326 2327 2328 2329 2330 2331 2332 2333 2334 2335 2336 2337 2338 2339 2340 2341 2342 2343 2344 2345 2346 2347 2348 2349 2350 2351 2352 2353 2354 2355 2356 2357 2358 2359 2360 2361 2362 2363 2364 2365 2366 2367 2368 2369 2370 2371 2372 2373 2374 2375 2376 2377 2378 2379 2380 2381 2382 2383 2384 2385 2386 2387 2388 2389 2390 2391 2392 2393 2394 2395 2396 2397 2398 2399 2400 2401 2402 2403 2404 2405 2406 2407 2408 2409 2410 2411 2412 2413 2414 2415 2416 2417 2418 2419 2420 2421 2422 2423 2424 2425 2426 2427 2428 2429 2430 2431 2432 2433 2434 2435 2436 2437 2438 2439 2440 2441 2442 2443 2444 2445 2446 2447 2448 2449 2450 2451 2452 2453 2454 2455 2456 2457 2458 2459 2460 2461 2462 2463 2464 2465 2466 2467 2468 2469 2470 2471 2472 2473 2474 2475 2476 2477 2478 2479 2480 2481 2482 2483 2484 2485 2486 2487 2488 2489 2490 2491 2492 2493 2494 2495 2496 2497 2498 2499 2500 2501 2502 2503 2504 2505 2506 2507 2508 2509 2510 2511 2512 2513 2514 2515 2516 2517 2518 2519 2520 2521 2522 2523 2524 2525 2526 2527 2528 2529 2530 2531 2532 2533 2534 2535 2536 2537 2538 2539 2540 2541 2542 2543 2544 2545 2546 2547 2548 2549 2550 2551 2552 2553 2554 2555 2556 2557 2558 2559 2560 2561 2562 2563 2564 2565 2566 2567 2568 2569 2570 2571 2572 2573 2574 2575 2576 2577 2578 2579 2580 2581 2582 2583 2584 2585 2586 2587 2588 2589 2590 2591 2592 2593 2594 2595 2596 2597 2598 2599 2600 2601 2602 2603 2604 2605 2606 2607 2608 2609 2610 2611 2612 2613 2614 2615 2616 2617 2618 2619 2620 2621 2622 2623 2624 2625 2626 2627 2628 2629 2630 2631 2632 2633 2634 2635 2636 2637 2638 2639 2640 2641 2642 2643 2644 2645 2646 2647 2648 2649 2650 2651 2652 2653 2654 2655 2656 2657 2658 2659 2660 2661 2662 2663 2664 2665 2666 2667 2668 2669 2670 2671 2672 2673 2674 2675 2676 2677 2678 2679 2680 2681 2682 2683 2684 2685 2686 2687 2688 2689 2690 2691 2692 2693 2694 2695 2696 2697 2698 2699 2700 2701 2702 2703 2704 2705 2706 2707 2708 2709 2710 2711 2712 2713 2714 2715 2716 2717 2718 2719 2720 2721 2722 2723 2724 2725 2726 2727 2728 2729 2730 2731 2732 2733 2734 2735 2736 2737 2738 2739 2740 2741 2742 2743 2744 2745 2746 2747 2748 2749 2750 2751 2752 2753 2754 2755 2756 2757 2758 2759 2760 2761 2762 2763 2764 2765 2766 2767 2768 2769 2770 2771 2772 2773 2774 2775 2776 2777 2778 2779 2780 2781 2782 2783 2784 2785 2786 2787 2788 2789 2790 2791 2792 2793 2794 2795 2796 2797 2798 2799 2800 2801 2802 2803 2804 2805 2806 2807 2808 2809 2810 2811 2812 2813 2814 2815 2816 2817 2818

PA (KOVA//) KOVALIC D K.
PA (ZUCH//) ZUCH V

PA (ZHOU//) ZHOU Y.
PA (CAOY//) CAO Y

FA (CA017) CA01.1.
XX

PI Kovalic DK, Zhou Y, Cao Y;

[illegible]

CC sequences mentioned in the specification and producing a plant having an
CC improved property. Producing a plant having an improved property
CC comprises transforming a plant with a recombinant construct comprising a
CC promoter region functional in a plant cell operably joined to a
CC polynucleotide comprising a coding sequence for a polypeptide associated
CC with the property, and growing the transformed plant. The polypeptide is
CC useful for improving plant cold tolerance, manipulating growth rate in
CC plant cells by modification of the cell cycle pathway, improving plant
CC drought tolerance, providing increased resistance to plant disease,
CC producing galactomanan (or lignin or plant growth regulators), improving
CC plant heat tolerance, improving plant tolerance to herbicides, increasing
CC the rate of homologous recombination in plants, improving plant tolerance
CC to extreme osmotic conditions or to pathogens or pests, improving yield
CC by modification of photosynthesis, modifying seed oil or protein yield
CC and/or content, improving yield by modification of carbohydrate, nitrogen
CC or phosphorus use and/or uptake, or improving yield by providing improved
CC plant growth and development under at least one stress condition. The
CC polynucleotide and polypeptide may also be used in recombinant DNA
CC constructs, in physical arrays of molecules, as plant breeding markers,
CC or in computer-based storage and analysis systems. The present sequence
CC is a Cotton plant cDNA of the invention. NOTE: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequences.html?docID=20040181330. However only 5885
CC polynucleotide sequences were available, the remaining 52213
CC polynucleotides and all 58798 protein sequences were not present.
XX
SQ Sequence 683 BP; 167 A; 155 C; 152 G; 209 T; 0 U; 0 Other;

Query Match 12.8%; Score 339.6; DB 13; Length 683;
Best Local Similarity 76.7%; Pred. No. 6.8e-81;
Matches 486; Conservative 0; Mismatches 129; Indels 19; Gaps 5;
1292 TTTTGAATCCTCTAGAAAGGCTTCTGTATTCTCTGTCCGCTCATGTCATGTGACCCA 1351
DB 52 TTTAAACCCCTCAAGGAAGGCTTTTGTATGTCATGCTGCTCATGCCACTGAACCCA 111
1352 GTGAAGCAGAGAGATTGCGCTTTTGTTCATCAGCTCTGGAAGAAATGAGTATTCAAAT 1411
DB 112 GTGAAGCAGAAAGCTTAAGTTCTTATCTGTCACACAGGGGGAAGGATGACTCAAT 171
1412 GGTAGTGTGAAGTCAGAGAGCTTTTGGAGATCATGGCCGAGTTTCATCAGCAAAAC 1471
DB 172 GGGTTGTTCAGTCAGAGAAAGTCTTCTGAGGTATGGCTGAGTCTCCCATCAGCAAAAC 231
1472 CCCTCTTGTGTGTCTTTGTGTCAGTAGCCCTCGCTTACCGCCTCGATACTATTCTA 1531
DB 232 CTCTCTTGTGTATTTTGTGTCAGTAGCTCTCTGTTACAGCCTCGTTATTCTA 291
1532 TCTCATCTCTCTAAGTTTGTCTCCCTCAAGAAATTCATGTCAGTGTGCTTTAGTATATG 1591
DB 292 TCTCATCTCTCCCTAGTGTGTACCTGCCAGGGTTTCATGTAACCTGCGCTTTAGTTATG 351
1592 GTCAAGCCCTACCGNAGGGTTCCAGGAGTGTTCGACATGATGAACGATGCAG 1651
DB 352 GTCAACTTCAACTGGAAGAAATTCACGGGGTGTGTCTCAACATGATGAAGAATGCAG 411
1652 TTCTCTCAGGA-----TAGCTGGGCTCTTATTTTGTTCGAACCTCAAACT 1696
DB 412 TTCTTTAGAAAGCAATGATTGATGTGGGCTCTTATTTATTCGCAATCCAAAT 471
1697 TCAAGTTACAGCTGACCCCTCAACTCCAAATTCATGTTGGGACCTGGTACAGGGTTAG 1756
DB 472 TTAAGCTCCCTGCAGATCCTTTCAGTTCCTTTCATCATGTTGGACCTGGGACCTGGATGG 531
1757 CTCTTTTCAGGATTTCTCGAGGAAGATGCGCTTCAGGAAATGTTGCTCAACTTG 1816
DB 532 CACCTTTCAAAGTTTCTTACA-GAAGATGTTGCTCTCAA-AAGATGTTGGAGAACTTG 589
1817 GCCCAGCAGTGTCTTTTTCGGATGTAGGAATCGTAAATATGAGCTTCATTTATGAAGACG 1876
DB 590 GCTCTTCTCTACTTTTGTGGATGAGGAATCGCA-ATGGATTTCATTTATGAAGATG 648

QY 1877 AACTAAACAATTCGTGGACGAGGAGTCATTTC 1910
DB 649 AGCT-CATAACTTGTGGACAAAGTGCCCTTTC 681
RESULT 15
ACN62895/c
ID ACN62895 standard; cDNA; 609 BP.
XX ACN62895;
XX ACN62895;
DT 02-DEC-2004 (first entry)
XX Cotton carpel wall/septum EST Clone ID: LIB3831-001-Q1-N6-F2, SEQ:17676.
DE Cotton; plant; EST; expressed sequence tag; transgenic plant;
XX carpel wall; septum; variety Nucotton33B; library LIB3831; molecular tag;
KW molecular marker; genetic mapping; molecular mapping; seed germination;
KW plant growth; plant quality; plant yield; plant breeding;
KW tissue printing; ss.
XX Gossypium hirsutum.
XX US2004123340-A1.
XX 24-JUN-2004.
XX 12-DEC-2001; 2001US-00021323.
XX 14-DEC-2000; 2000US-0255619P.
XX (DEIK/) DEIKMAN J.
PA (FENG/) FENG P C C.
PA (FINC/) FINCHER K L.
PA (ZIEG/) ZIEGLER T E.
XX Deikman J, Feng PCC, Fincher KL, Ziegler TE;
XX WPI; 2004-479808/45.
XX New isolated nucleic acid molecule that encodes a plant protein or its
PT fragment, useful for isolating a variety of agronomically significant
PT genes associated with plant growth, quality or yield, and as molecular
PT tags to map genes.
XX Claim 1; SEQ ID NO 17676; 34pp; English.
XX The invention relates to 17880 cotton expressed sequence tags (ESTs;
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated
CC from primed or non-primed seeds from variety DP50B, mature seeds from
CC variety Coker 312 Boswell 96 Field, and androecium tissue, Gynoecium
CC tissue, developing fibres, carpel walls and septa from variety
CC Nucotton33B. The invention also relates to substantially purified
CC proteins or their fragments encoded by nucleic acid molecules of the
CC invention, and to transformed plants having a nucleic acid construct
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as
CC molecular tags to isolate genetic regions, to isolate genes, to map
CC genes, to determine gene function and to determine whether genes are
CC members of a particular gene family. The nucleic acid molecules may be
CC used for isolating a variety of agronomically significant genes
CC associated with plant growth, quality, yield, and could also serve as
CC links in metabolic and catabolic pathways. The nucleic acid molecules are
CC also useful for identifying genes important in initiating and maintaining
CC seed germination or that may be used to mitigate stresses encountered
CC during seed germination. The ESTs additionally enable the acquisition of
CC promoters and cis-regulatory elements which will be useful to express
CC agronomically significant genes in these tissues and/or other tissues,
CC and also permits the acquisition of molecular markers useful in breeding
CC schemes, genetic and molecular mapping, and in cloning of agronomically
CC significant genes. The nucleic acid molecules are further useful for
CC detecting the expression level or pattern of a protein or mRNA and for
CC detecting the presence or quantity of a protein by tissue printing. The
CC present sequence represents a specifically claimed EST isolated from a

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APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; LENGTH: 2755		
; TYPE: DNA		
; ORGANISM: Glycine max		
; FEATURE:		
; OTHER INFORMATION: Clone ID: PAT_MRT3847_140138C.1		
; US-10-424-599-44452		
Query Match 40.7%; Score 1079; DB 18; Length 2755;		
Best Local Similarity 74.6%; Pred. No. 5.9e-271;		
Matches 1404; Conservative 0; Mismatches 460; Indels 19; Gaps 3;		
QY	311	TAATTGATAAAGAGAGAGAGATTGAAGTTGATCCTGGTAAATTAAGCTCACATATAT 370
DB	446	TGAAGGAAGAAGAAGACGAAGTCGATCGTCTGGTGGGAAGACCCGAGTTGCCATTT 505
QY	371	TTTTTGGTACTAGACTGGTACTGCTGAGGATTGCTTAAGGATTCGGCAGGAAGAAATTA 430
DB	506	TCTTCGGAATCAAACTGGTACCGCTGAGGCTTTGCCAAGGCTTTGGCAGAGAGATCA 565
QY	431	AGCAAAAGTACAAGAACGAGTTGTTAAAGTAGTTGACCTGGATGACTATGCAGCCGAGG 490
DB	566	AGCTAGGTATGAAGAAGCAGCTGTCAAGTTGCTGACCTGGATGACTATGCAATGGATG 625
QY	491	ATGATCAATATGAAGAGAAATTAAGAAAGAGTCTTTTGGTGTGTTTTTCATGGTAGCCACTT 550
DB	626	ATGATCAATATGAAGAGAGCTGAAGAAAGAGTCACTTGCAATTTTTCATGTTGGCAACAT 685
QY	551	ATGGTATGTGAGCCAACTGACAAATGCTGCGAGATTTTACAATGGTTCACTCAGG--- 607
DB	686	ATGGAGATGGAGGCCAACTGACAAATGCTGCAAGATTCTACAATGGTTTACTGAGGGTA 745
QY	608	AACATGAAGGGGAGAGTGGCTTCAGCACTACTTATGGTGTGTTTTGGTTGGTTAAACC 667
DB	746	AAGCAGAGGGGTATCTGGCTTCA-CAGCTCAGTATGGTGTGTTTTGGCTTAGGTAACC 804
QY	668	GTCAATACGAGCATTTTCAACAAGATCGCGTAGATGTGATGAGCAACTCGGTAAACAAG 727
DB	805	GGCAATATGAACATTTTAAGAAGTAGTAAATAGTTGATGAAGAACTTAGTGAGCAAG 864
QY	728	GTGCAAGCGCATGTTTCAAGTGGGCTCGGTGACGATGATCAATGATGATGAAGATGATT 787
DB	865	GTGCAAGCGCTTGTGTTCCATTGGGACTAGGTGATGACGATCAATCCATTGAGGATGATT 924
QY	788	TTACTGCTGGCAGAAATGTTCTGGACTGAAATGGATCAGTTGCTCAAGATGAGGATG 847
DB	925	TTGTTGCTTGGAGGAATCTCTATGGTCTGAGTTGGATCAGTTGCTCCGGGATGAGGATG 984
QY	848	CTGCTCTCTCAGTGGGTACACCGCTATATTTGCTACTGTTCTGTAATACAGGGTAGTATT 907
DB	985	ATGTAATACTGTATCTACTCTTATAAGGCTGCTATTCTGTAATTCGAGTGTATTTC 1044
QY	908	ACGAAACTACGGTGGGCTCTGGATGATAAACAATAATCTGTAACGGCGATGTTG 967
DB	1045	ATGATCCACCGTCACATCTGCAATGATAATCACTTAAATGGCAATGGTAATGCTG 1104
QY	968	CATTTGATATCTCCATCTCTGAGAACCACTTGTGCTCAACAAGAGAGCTCCACAAC 1027
DB	1105	TGTTTGATATTCACCATCTCTGAGGGTTAATATGCGGCTCAAGAGAACTTCAACAAC 1164
QY	1028	CCAAGTCTGATAGATCTGTATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACAT 1087
DB	1165	CTGAGTCTGATCGTTCTTGATACATTTGGAGTTTGACATATCCGGGACTGGCATATAT 1224
QY	1088	ATCAGACTGGAGATCATGTTGGTGTATGCTGAGAACTGCGATGAACCTGTCGAGGAAG 1147
DB	1225	ATGAAACTGCTGACCATGTGGGTGTTTTGCTGAAAACGCGCATGAACTGTTGAAGAAG 1284
QY	1148	CAGGAGACTGTTGGGTCAACCCCTGGATTGCTGTTTTCAATTCACCGGATAAGAAG 1207
DB	1285	CTGGAAGTTGCTGGGTGAGGATTTAGATTGGTATTTTCCATTCACTCAATAATAGAG 1344
QY	1208	ACGGGTACCCCGGAGGAGCTCATTTACCACTCTCTTCCAGGTCTTGCACCTTACGAT 1267

RESULT 3

US-10-425-115-98408
; Sequence 98408, Application US/10425115
; Publication No. US2004021427A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants
 ; FILE REFERENCE: 38-21(53222)B
 ; CURRENT APPLICATION NUMBER: US/10/425,115
 ; CURRENT FILING DATE: 2003-04-28
 ; NUMBER OF SEQ ID NOS: 369326
 ; SEQ ID NO 98408
 ; LENGTH: 2892
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: MRT4577_21258C.1
 US-10-425-115-98408

Query Match 34.1%; Score 904; DB 20; Length 2892;
 Best Local Similarity 68.5%; Pred. No. 3.8e-225;
 Matches 1287; Conservative 0; Mismatches 570; Indels 21; Gaps 2;
 QY 319 AAGAAGAGAGAGATTGAAGTTGATCTCTGGTAAATTAAGCTCACTATATTTTTGGT 378
 DB |||||
 QY 319 AAGGTGACGCCGACGCGAGTTGATGACGCGCGAAGCGCTCACCATCTTCTTCGGC 378
 DB |||||
 QY 379 ACTCAGACTGGTACTGCTGAGGATTTGCTAAGGCATTGGCAGAGAATAAAGGCAAG 438
 DB |||||
 QY 379 ACACAGACTGGCACCCCGAGGGGTTGCGCAAGTCCATGGCGAGGAGCGGCGCG 438
 DB |||||
 QY 439 TACAAGAAAGCAGTTGTTAAAGTAGTTGACCTGGATGACTATGCAGCGAGGATGATCAA 498
 DB |||||
 QY 439 TACGAGAGCCGTTGTCAAAGTTGGTGATCTGGATGACTATGCTCAGGAGGACGAGGAA 498
 DB |||||
 QY 499 TATGAAGAGAAATTAAGAAGAGTCTTTGGTGTCTTTTCATGGTAGCCACTTATGGTAT 558
 DB |||||
 QY 499 TACGAGAGAGAGCTGAAGAAGGAACTGTGGTGTCTTCTCTAGCAACATATGGGAT 558
 DB |||||
 QY 559 GGTGAGCCACTGACATGCTGCGAGATTTTACAATGGTTCACTCAGGAAACATGAAGG 618
 DB |||||
 QY 559 GGGAGCCCACTGATTAATGAGCAGCATTTCTACAAATGGTTTACTCAGGGAAGAGAAAG 618
 DB |||||
 QY 619 GGAGAGTGGCTTCAGCAACTAACTTATGGTGTCTTTGGTGTGGTAAACCGTCAATACGAG 678
 DB |||||
 QY 619 GAAGTTGGCTGAAGGATCTTAATATGGTATTTTGGCTTGGAAACAGGCAATACGAA 678
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 QY 679 CATTTCAACAAGATCGGGTAGATGGATGAGCAACTCGGTAAACAAGGTGCAAGCGC 738
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 QY 679 CATTTTAATAAGGTTGCAAGGTTGGTAGATGAGCTAGTAGAGGAGCAGGTTGGGAAACGT 738
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 QY 739 ATTGTTCAAGTGGGCTCGGTGACGATGATCAATGCAATGCAATGATTTACTGCTTGG 798
 DB |||||
 QY 739 CTGTGCTCTGTTGGCTTGGAGACGATGATCAGTGCATTTGAGGATGATTTCACTGCAATGG 798
 DB |||||
 QY 799 CGAGAATTTGTGGACTGAATTTGGATCAGTTGCTCAAAAGATGAGGATGCTGCTCTTCA 858
 DB |||||
 QY 799 AAGAAGTAGTGTGCGCAGAAATTTAGATCAATTTGCTCCGCAAGAGATGACCAACTGGT 858
 DB |||||
 QY 859 GTGGCTACACCGPATATGCTACTGTTCTCTGTAATACAGGGTAGTGAATCAGCAAACTACG 918
 DB |||||
 QY 859 GCATCGACTCCATATACTGCTGCTATTTCTGTAATACAGAGTTGTTTTCATTGCAAACTCT 918
 DB |||||
 QY 919 GTCCGGCTCTGGATGATAAACAATTAATGCTTAACCGGATGTTGCAATTTGATATT 978
 DB |||||
 QY 919 GACCTGTCAATCCAAAGATGATCATGGACACTAGCAACCGGTACTGGTGTGATTTGATATT 978
 DB |||||
 QY 979 CTCATCTCTTGCAAGAACCTTTGTTGCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGAT 1038
 DB |||||
 QY 979 CAACACCTTGCAGGCTTAATGTTGCTGTTTCGGAAGAGCTGCACAAACGAGCTTCAGAT 1038
 DB |||||
 QY 1039 AGATCTGTATACATCTGGAGTTTCGATATACAGGCTCTTCCCTTACATATGAGACTGGA 1098
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 QY 1039 CGCTCTGTATCATCTCGAGTTTGACATTTCTTGGCACTGGTCTTGTGTATGAACCGGA 1098
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QY 1099 GATCATGTTGGTGTGTTTATGCTGAGAACTGTCGAGAAAGCAGGGAAGCTG 1158
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 QY 1099 GACCATGTTGGTGTATATCAGAAAATCTGTTGACACTGTGGAGAGGTTGAAGGCTA 1158
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 QY 1159 TTGGGTCAACCCCTGATTTGTTTCAATTCACACGGATAAAGAACGCGGTCAACCC 1218
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 QY 1159 CTTGACCTTTCTCCAGACACATCTTCTCCATCCATGAGATGCAAGATGATTCCT 1218
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 QY 1219 C-----AGGGAAGCTCATTAACACCTCTTTCCAGGTCCTTTGACCTTACGATCTGCC 1272
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 QY 1279 CTTCTACGATATGCTGATCTACTCAATCCACGAAGAAGGCTGCTTTGCTTGTAGCT 1338
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 QY 1333 GCTCATGCTATCTGTACCCAGTGAAGCAGAGAGATTGCGGCTTTTGTGTCATCACCTCTGGGA 1392
 DB |||||
 QY 1339 TCTCAGCATCTGATCCAGCTGAGCTGAGCACTTAGATTTCTTGGCTTCTCTCTCGGA 1398
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 QY 1393 AAGAAATGAGTATTTCAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGGCC 1452
 DB |||||
 QY 1399 AAGGATGAGTATTTCTCAATGGATAACTGCTAGTCAGAGGAGCTTCTTGAAGTTATGGCC 1458
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 QY 1453 GAGTTTCCATCAGCAAAACCCCTCTTGTGTGTTCTTTGCTGCGAGTAGCCCTCGCTTA 1512
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 QY 1513 CGGCTCTGATATCTATCTCATCTCTCTCAAGTTTGTCTCCCTCAAGAAATTCATGTG 1572
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 QY 1519 CAACCAAGATATCTCAATTTCACTCAATGCTCAGAGTGGCTCCCTCCAGAAATTCATGTA 1578
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 QY 1579 ACATGTGCTTATGTTTATGGGCTTTCACCAACAGGAAGGATCCACCAAGGAGTTTGTTC 1638
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 QY 1678 TTTGTTTCAAGCTCAAACTTCAAGTTTACAGCTGAGCCCTCAACTCCAATTTATCATGGTG 1737
 DB |||||
 QY 1699 TTTGTGAGCAGTCAAAATTTCAAGTTTACCTGCTGATCCGCTCACTCTATATCATGAT 1758
 DB |||||
 QY 1738 GGACCTGTGATAGGTTAGTCTCTTTGAGAGATTTTCGAGAAAGAAATGCGCCCTCAAG 1797
 DB |||||
 QY 1759 GGTCTGAGCAGGCTGCTCTTTAGAGGCTTCTTTCAGGAAAGGTTAGCAATGAAA 1818
 DB |||||
 QY 1798 GAAATGGTGTCTCAACTGGGCGCAGAGTCTTTTTCGATGTAGGATCGTAAATATG 1857
 DB |||||
 QY 1819 CAATCTGGGCGAGAAATTTGGGCACCTTCAATCTTTTTCGATGCGAGAACCGTAAATATG 1878
 DB |||||
 QY 1858 GACTTCATTTATGAAGACGAACCTTAACTTTCGTAACGAGGAGTCAATTTCCGAGCTA 1917
 DB |||||
 QY 1879 GACTACATATATGAAGATGAGTTGCAAACTTTCTTGGAGAGGGGCGCTTCTGAGCTA 1938
 DB |||||
 QY 1918 GTTATGCTTTTCAAGTGAAGGAAAGAGGAATATGTTTCAACATGAAGATGAGAG 1977
 DB |||||
 QY 1939 ATTGTTGATTTCTCTCGGAAGGGCAACGAAGAATAATGTGCGACATAAGATGTTGGAA 1998
 DB |||||
 QY 1978 AAGCAACGGATGATGGAATGATATCAGGGGACGGTTATCTCTATGTGTGTGAT 2037
 DB |||||
 QY 1999 AAGGCCACAGATATTTGGAACATCATCTCAATGTTGTTTACTTATATGTTTGGCGTGAT 2058
 DB |||||
 QY 2038 GCCAAGGGAATGGCCAGAGATGCTCCATCGCACTTTCATACCAATTTGCCCAAGGAAACAGGGA 2097
 DB |||||
 QY 2059 GCCAAGGGAATGGCTAGAGATGTACACAAAATGCTTCAACAAATAGTCCAGAGCAGGGA 2118
 DB |||||
 QY 2098 CCCATGGAATCATCTGCTGCGCAAGCTGAGTAAAGAAATCTCCAAGTTGGAAGACGATAT 2157
 DB |||||
 QY 2119 TCTTTGGATTAATCTCAAAACCGAGAGCTATGTAAAGAGCCTCGAGATGGAAGGAGGTAC 2178
 DB |||||
 QY 2158 CTAAGAGATGTCTGGTGA 2175

QY 1691 CAAACTTCAAGTTACAGCTGACCCCTCAACTCAATTATCATGGTGGAGCCTGGTACAG 1750
DB 1652 CCAACTTCAAGTTCTCTCTGATTTAAGGTACCGATCATCATGATCGGTCCAGGACTG 1711
QY 1751 GGTAGCTCTCTTTCAGAGGATTTCTGAGGAAAGATGGCCCTCAAGAAATAGTCTC 1810
DB 1712 GATTAGCTTCAATTCAGAGGATTTCTTCAAGGAAAGACTAGCGTTGGTAGAATCTGGTGTG 1771
QY 1811 AACTTGGCCCAAGCAGTGTCTTTTTCGATGTAGGAATCGTAATATGCACTTCATTTATG 1870
DB 1772 AACTTGGCCCATCAGTTTGTCTTTTGGATGCAGAAACCCGTAAGATGGAATTCATCTACG 1831
QY 1871 AAGACGAACCTAAACAACTTCTGTGAACGAGGAGTCAATTCGGAGCTAGTTATTGCCCTTTT 1930
DB 1832 AGGAAGAGCTCCACGGATTTGTTGAGAGTGGTCTCTCGAGAGCTAAGTGTGCGCTTCT 1891
QY 1931 CACGTGAAGGGGAAAGAGGAATATGTTCAACATAAGATGATGAGAGAAACGAGATG 1990
DB 1892 CTCGTGAAGGACCCACCAAGAAATACGTACAGCAACAAGATGATGCAAGGCTTCTGATA 1951
QY 1991 TATGGAATGTGATATCAGGGGACGGTATCTCTATGTGTGTGGTATGCCAAGGAGATGG 2050
DB 1952 TCTGGAATATGATCTCTCAAGGAGCTTATTATATGTTTGTGTGACGCCAAGGAGCATGG 2011
QY 2051 CCAGAGATGTCATCGCACGTTGTCATACCAATTCGCCAAGAACAGGGACCCATGGAATCAT 2110
DB 2012 CAAGAGATGTTACAGATCTCTCACACATAGCTCAAGAACAGGGGTCAATGGATCAA 2071
QY 2111 CTGCTGCGGAGCTGAGTAAAGAACTCCAAAGTTGAAGAACGATATCTAAGAGATGCT 2170
DB 2072 CTAAGCAGAGGGCTTCGTGAAGAACTCTGCAACGAGTGGGAAGATATCTTTAGAGATGAT 2131
QY 2171 GGTGA 2175
DB 2132 GGTAA 2136

RESULT 6

US-09-938-842A-803
; Sequence 803, Application US/09938842A
; Publication No. US20040009476A9
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Klops, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SRIPI300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 803
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-803

Query Match 33.8%; Score 895.4; DB 11; Length 2136;
Best Local Similarity 67.3%; Pred. No. 5.6e-223;
Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;
QY 206 TCATTATGTCACAACTGTAGCTTCAATGCTGATTGGAATTTGTTCTTCGCAATGATGA 265
DB 161 TGATTGTTACCACTTCCATTGCTGTTCTTATTGTTGATCGTTATGCTCGTTTGGAGGA 220

QY 266 AATCTTCGTCTTCTCAATCAAAACCTATTGAAACTTATAAAACCAATAAATTGATAAAGAAG 325
DB 221 GATCCGGTCTCGGAATTCAAAACGCTGTCGAGCTCTTAAGCCCTTTGGTTATTAAAGCCTC 280
QY 326 AAGAGAGATGTAAGTTGATCTCTGGTAAAAATTAAGCTCACTATATATTTTGGTACTCAGA 385
DB 281 GTGAGGA---AGAGATTGATGATGGGCGTAAGAAAGTTACCATCTCTTTTCCGTACACAAA 337
QY 386 CTGGTACTGCTGAAGGATTTGCTAAAGCATTTGCGACGATGTCGACGAGAAATTAAGGCAAGGTACAGA 445
DB 338 CTGGTACTGCTGAAGGTTTTCAGAGGCTTTAGGAGAAAGCTTAAAGCAAGATATGAAA 397
QY 446 AAGCAGTGTGTAAGTAGTTGACCTCGATGACTATGACGCCGAGGATGATCAATATCAAG 505
DB 398 AGACCAAGATTCAAAATCGTTGATTTGGATGATTAACGGGCTGATGATGATGATGATGAGG 457
QY 506 AGAAATTAAGAAAGAGTCTTTGGTGTGTTTTCATGTTAGTGCACCTATATGTTGATGGTGAAGC 565
DB 458 AGAAATTTGAAGAAAGAGGATGTCGCTTTCTTCTTCTTAGCCACATATGGAGATGGTGAAGC 517
QY 566 CAACTGACATGCTGCGAGATTTTACAAATGGTTCACCTCAGGAACATGAAGGGGAGAT 625
DB 518 CTACCCACATGACGAGATTTCTCAAAATGGTTCACCGAGGGGAATGACAGAGGAGAAAT 577
QY 626 GGCTTCAGCAACTAACTTATGGTGTGTTTGGTTTGGTAAACCGTCAATACGAGCATTTCA 685
DB 578 GGCTTAAGAACTTGAAGTATGGAGTGTGTTGGATTTAGGAACACACATATGAGCATTTTA 637
QY 686 ACAAGATCGCGTGAAGTGTGGATGAGCAACTCGGTAAACAAAGGTGCMAAGCGCATTTGTTTC 745
DB 638 ATAAGGTTGCAAAAGTTGTAGATGACATCTTCTGCAACAAAGGTGCACAGCGCTTGTGAC 697
QY 746 AAGTGGGCTCGGTGACGATGATCAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 805
DB 698 AAGTGGTCTTGGAGATGATGACACAGTGTATGGAAGTGAATTTACCGCTTGGCGAAG 757
QY 806 TGTGTGGACTGAATTTGGATCAGTGTCTCAAGATGAGGATGCTGCTTCTTCAAGTGCTA 865
DB 758 CATTTGGCCCGAGCTTGTATACATATCTGAGGAGAGAGGGGATACAGCT---GTTGCCA 814
QY 866 CACCGTATATGCTACTGTTCTGAAATACAGGGTGTGATGATTCACGAAACTACCGTCCGCG 925
DB 815 CACCATACACTGCGCTGTGTTAGAATACAGAGTGTCTTATTCACGACTCTGAAAGATGCCA 874
QY 926 CTCTGGATGATTAACACATAAATACTGCTTAAACGGCGATGTTGATGATGATGATGATGATGAT 985
DB 875 AATTCATGATATAAACTGGCAATGGGAAATGGGAAATGGTGTGTTGATGCTCAACATC 934
QY 986 CTTGCAAGAACCATTTGTTGCTCAAAAGAGAGCTCCACAAACCCAAAGTCTGATAGATCCT 1045
DB 935 CTTACAAAGCAATGTGCTGTTTAAAGGGAGCTTCACTACTCCGAGTCTGATCGTCTCTT 994
QY 1046 GTATACATCTGGAGTTGACATATCAGGCTCTTCCCTTACATATGATGATGATGATGATGATGATG 1105
DB 995 GTATCCATTTGGAATTTGACATTTGCTGGAAGTGGACTTACGTTATGAACTGGAGATCATG 1054
QY 1106 TTGGTGTGTTTGTGAGAACTGGATGAACTGTGTCGAGGAGGAGGAGGAGCTGTTGGGTC 1165
DB 1055 TTGGTGTACTTTGTGATAACTTAAAGTGAACCTGTAGATGAAGCTCTTAGATGCTGGATA 1114
QY 1166 AACCCCTGGATTTGCTGTTTTCATTCACACGATAAAGAGACGGGTCAACCCAGGGAA 1225
DB 1115 TGTCACCTGATTAATTTCTACTTCACGCTGAAAGAGACGGCACCAATCAGCA 1174
QY 1226 GCTCAATTAACACCTCTCTTCCAGGCTCTTGCACCTTACGATCTGCCCTAGCACGCTATG 1285
DB 1175 GCTCACTGCTCTCTCTCTTCCCA---CTTGCACAACTTGAGAACAGGCGCTTACACGATATG 1231
QY 1286 CTGATCTTTTGAATCTCTCTAGAAAGGCTCTCTGATGCTCTGCTCGGCTCATGATCTG 1345
DB 1232 CATGCTTTTGTGATTTCTCCAAAGAGTGTGCTTTAGTTGCTGTTGGCTGCTCATGCTG 1291
QY 1346 TACCCAGTGAAGCAGAGAGATTTGCGCTTTTGTGTCATCACCTCTGGGAAAGATGATGATTT 1405

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Db 1292 ATCTACCGAAGCAGAACGATTAACACCTGCTTACCTGCTGGAAGGATGAATATT 1351
Qy 1406 CAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGGCCGAGTTTCCATCAG 1465
Db 1352 CAAAGTGGGTAGTAGAGTCAAGAGTCTACTTGAGGTGATGGCCGAGTTTCCITCAG 1411
Qy 1466 CAAAACCCCTCTTGGTGTGTTCTTTGCTGAGTAGCCCTCGCTTACCGCCCTCGATCT 1525
Db 1412 CCAAGCCACCACTTGGTGTCTTCTGCTGAGTTGCTCCAAGGTGTCAGCCTTAGTCT 1471
Qy 1526 ATTCTATCTCATCTCTCCCTAAGTTTGTCTCCCTCAAGAAATTCATGTGACGTGTCTTAG 1585
Db 1472 ATTCTGATATCATCTGCCCAAGATGCTGAAACTAGAAATTCACGTCAAGTGTGCACTGG 1531
Qy 1586 TATATGCTCAAGCCCTTACCGGAAGGTTTCCAGGAGAGTGTGTTCCACATGATGAAGC 1645
Db 1532 TTTATGAGAAATGCCAACTGGCAGGATTCATAAGGGAGTGTGTTCCACTTGGATGAAG 1591
Qy 1646 ATGAGTTCCTCAGGA-----TAGCTGGGCTCCTATTTTGTGTTGCGAACGT 1690
Db 1592 ATGCTGTGCCCTTACGGAAGAGTGAAACTGTCTCGGCGCGATATTTGTTAGGCAAT 1651
Qy 1691 CAAACTTCAAGTTACCAAGCTGACCCCTCAACTCCAATTATCATGTGGGACCTGGTACAG 1750
Db 1652 CCACTTCAAGCTTCTCTTCTGATTTAAGGTACCGATCATCATGCTGGTCCAGGACTG 1711
Qy 1751 GGTAGCTCTCTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGAAATGGTGCTC 1810
Db 1712 GATTAGCTCATTCAGAGGATTCCTTCAGGAAAGACTAGCGTTGGTAGAATCTGGTTG 1771
Qy 1811 AACTTGGCCAGCAGTGTCTTTTTCGGATGTAGGAATCGTAATATGGAATCTCATTTATG 1870
Db 1772 AACTTGGGCCATCAGTTTGTCTTCTTGGATGCGAAGAACCCGTAGAATGGAATTCATCAG 1831
Qy 1871 AAGACGAATCAACACTTCGTGCGACGAGGTCACTTTCGGAGCTAGTTATTCGCTTTT 1930
Db 1832 AGAAGAGCTCCAGCGATTTGTTGAGAGTGGTGTCTTCGCAGAGCTAAGTGTGCGCTTCT 1891
Qy 1931 CAGGTGAAGGGGAAAAGAGGAATATGTTCAACATAAGATGATGGAAGAACCAACGGATG 1990
Db 1892 CTCGTGAAGGACCACCAAGAAATACGTACAGCACAAGATGATGGACAAGGCTTCTGATA 1951
Qy 1991 TATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGTGATGCCAAGGGAATGG 2050
Db 1952 TCTGGAATATGATCTCTCAAGGAGCTTATTTATATGTTTGTGTGACGCCAAGGCAATGG 2011
Qy 2051 CCAGAGATGTCCATCGCACGTGTCATACCATTCGCCAAGAACAGGACCCCATGGAATCAT 2110
Db 2012 CAAGAGATGTTCAGATCTCTCCACAAATAGCTCAAGAACAGGGGTCAATGGNTTCAA 2071
Qy 2111 CTGCTCGGAGCTGCAAGTAAGAAACTCCAAGTTGAAGAACGATATCTAAGAGATGTCT 2170
Db 2072 CTAAGCAGAGGGCTTCGTGAAGATCTGCAACGAGTGTGAAGATATCTTAGAGATGTAT 2131
Qy 2171 GGTGA 2175
Db 2132 GGTAA 2136
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RESULT 7

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US-11-069-633-13
; Sequence 13, Application US/11069633
; Publication No. US20050208643A1
; GENERAL INFORMATION:
; APPLICANT: Schmidt-Dannert, Claudia
; APPLICANT: Watts, Kevin
; TITLE OF INVENTION: Flavonoids
; FILE REFERENCE: 09531-160001
; CURRENT APPLICATION NUMBER: US/11/069,633
; CURRENT FILING DATE: 2005-03-01
; PRIOR APPLICATION NUMBER: US 60/549,077
; PRIOR FILING DATE: 2004-03-01
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; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 2136
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-11-069-633-13
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Query Match 33.8%; Score 895.4; DB 24; Length 2136;
Best Local Similarity 67.3%; Pred. No. 5.6e-223;
Matches 1335; Conservative 0; Mismatches 626; Indels 24; Gaps 4;
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Qy 206 TCATTATGTCACAACCTGTAGCTTCAATGCTGATTTGGTATTTGTTCTTCGTCATGTATGA 265
Db 161 TGAATGTTACCACTTCCATTGCTGTTCTTATTTGGTTGTCATGTTATGCTGTTGGAGGA 220
Qy 266 AATCTTCGTTCTTCAATCAAAACCTTATTGAAACTTATAAACCAATAAATTGATAAAGAA 325
Db 221 GATCCGGTTCTGGGAATTCAAAACGTCGAGCCCTTTAAGCCTTTGGTTATTATTAAGCCTC 280
Qy 326 AAGAGGAGATTGAAGTTGATCCTGTGTAATAAATAAGCTCACTATATTTTTTGTGTACTCAG 385
Db 281 GTGAGGA---AGAGATTGATGATGGCGTAAGAAAGTTTACCATCTTTTCGGTACACAAA 337
Qy 386 CTGGTACTGCTGAAGATTTGCTTAAGGCATTTGCGACAGAAATTAAGGCAAGTACACAAGA 445
Db 338 CTGGTACTGCTGAAGGTTTTTGCAAAAGGCTTTTAGGAGAAGAAAGCTAAAGCAAGATATGAA 397
Qy 446 AAGCAGTCTGTTAAAGTAGTTGACCTGATGACTATGCGACCGAGGATGATCAATATGAAG 505
Db 398 AGACCAGATTCAAAATCGTTGATTTGGATGATTAACGGCTGATGATGATGATGATGAGG 457
Qy 506 AGAAATTAAGAAAGAGTCTTTTGGTGTTTTTCATGGTAGCCACTTATGTGATGTTGTGAGC 565
Db 458 AGAAATTAAGAAAGAGGATGTGGCTTTCTTCTTTAGCCACATATGAGATGTTGTGAGC 517
Qy 566 CAACTGACAAATGCTGCGAGATTTTACAAATGTTTCACTCAGGNAACATGAAGGGGAGAGT 625
Db 518 CTACCCACAAATGCGCGAGATTTCTACAAATGTTTCCAGGGGGAATGACAGAGGAGAAT 577
Qy 626 GGTCTCAGCAACTAACTTATGTTGTTTGGTAACTGCTCAATACGACGATTTTCA 685
Db 578 GGTCTAAGAACTTGAATGAGTGTGTTGGATAGGAAACAGACAAATATGACATTTTA 637
Qy 686 ACAAGATCCGGTGTAGATGTGATGAGCAACTCGGTAAACAAGGTGCAAGCGCATTTGTTTC 745
Db 638 ATAAGGTTGCCAAAAGTTGTAGATGACATTTCTGTCGAACAAGGTGACACGCGCTTTGTAC 697
Qy 746 AAGTGGGGCTCGGTGACGATGATCAATGATTCAGATGATTTTACTGCTTGGCGAGAAT 805
Db 698 AAGTTGGTCTTGGAGATGATGACCAAGTGTATTGAAGATGACTTACCGCTTGGCGAGAAG 757
Qy 806 TGTGTGGAAGTCAATTTGGAATCAGTTGCTCAAAAGATGAGGATGCTGCTTTCAGTGGCTA 865
Db 758 CATTTGGCCCGAGCTTGTATACAACTACGAGGGAAGAGGGGATACAGCT---GTTGCCA 814
Qy 866 CACCGTATATGTCTACTGTTCTCGAATAACAGGGTAGTGTATTCAGAAACTACGTCGCGG 925
Db 815 CACCATACACTGCAGCTGTGTTAGATAACAGAGTTTCTATACCGACTCTGAAGATGCCA 874
Qy 926 CTCTGGATGATAAACACATATAATACTGCTAACCGGATGTTGATTTGATTTCTCCATC 985
Db 875 AATTCAATGATATAAACATATGGCAAAATGGGAATGTTTACTGTGTTGATGCTCAACATC 934
Qy 986 CTTTGCAAGAACCAATTTGTGCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGTAGATCTCT 1045
Db 935 CTTACAAAGCAAAATGTGCTGTTTAAAGGGAGCTTCACTACTCCCGAGTCTGATCGTTCTT 994
Qy 1046 GTATACATCTGGAGTTGACATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATG 1105
Db 995 GTATCCATTTGGAATTTGCAATTTGCTGGAAGTGGACTTACGTATGAACTGGAGATCATG 1054
Qy 1106 TTGGTGTTTTATGCTGAGAACTGCGATGAAACTGTTCGAGGAAGCAGGGAAGCTGTTGGTCT 1165
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Db 1218 GGGGAAGCGCTTGTGCCAGTGGGTCTAGGTGATGATCAATGCAATTGAGGATGACT 1277
Qy 788 TTACTGCTCGCGAGAAATGTTGTGGACTGAAATGGATCAGTTGCTCAAGATGAGGATG 847
Db 1278 TTACTGATGAAAGAAAGAACTGTGGCCAGCATTTGGATGAATTTGCTTAGAGATGAGGACG 1337
Qy 848 CTGCTCCTTCAGTGGGTACACCGGTATATTTCTACTGTTTCTGTAATACAGGGGTAGTGATTC 907
Db 1338 ATGCAACT---GTGCTACACCTTATCTGCTGCACTTTTGGAGTACCGGGTGTATTTC 1394
Qy 908 ACGAAATACGGTCGGCGCTCTCGATGATGATAAACAATACTGCTAAACGGCGATGTTG 967
Db 1395 ATGATCCATTGGAAGCATCTGTGCGACGAAAGAAAGTGGCATAATGTAATGGTCACGCCA 1454
Qy 968 CATTTGATATTTCCATCCTTGCAGAACCAATGTTGCTCAACAAAGAGAGCTCCACAAC 1027
Db 1455 TTGTGGATGTTCAACATCCAGTCAAGGCAATGTGGCTGTGAAAGGAGCTTCATACTC 1514
Qy 1028 CCAAGTCTGATAGATCCTGTATACATCTGGAGTTTGCACATATCAGGCTCTTCCCTTACAT 1087
Db 1515 CTGCACTCTGATCGATCTTGCACTCAITTTGGAATTTGACATTTTCAAGCACTGGAGTTACAT 1574
Qy 1088 ATGAGACTGAGATCATGTTGGTGTATATCTGAGAACTCGCATGAAACTGTGCGAAG 1147
Db 1575 ATGAAACTGGGGACCATGTTGGTGTATTTACTGTGAGAAATTTGTCTGAAACTGTGGAAGAG 1634
Qy 1148 CAGGGAAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTCCAAATTCACCGGATAAAGAAG 1207
Db 1635 CAATAGGTTAATAGGTTTGTCCACGATACCTATTTCTCAATCCATACCTGATGATGAAG 1694
Qy 1208 ACGGGTCAACCCAGGGAAGCTCAITACCACTCCTCTTCCAGGCTCTTGCAACCTTACGAT 1267
Db 1695 ATGCAACACCACTAGCGGAAGCTCCTTGCCACCTACATTTCCCACTGTACTCTAAGAA 1754
Qy 1268 CTGCGCTAGCAGTATGCTGATCTTTTGAATCCTCTGAGAAAGGCTTCTCTGATGCTC 1327
Db 1755 CAGCACTTGCAATATGCAATGTTTGTAGTTTCAACCAAAAGTCTGCGCTTGGCT 1814
Qy 1328 TGTCCGCTCATGATCTGTACCACTGTAAGCAGAGATTTGCG-CTTTTGTCTATCACCT 1386
Db 1815 TAGCTGCTCATGATCTGATCCATCTGAACTGATCGACTAAGACATCTTCGGCTCACCT 1874
Qy 1387 CTGGGAAGATGAGTATTCAAATGGGTAGTTTGGAAAGTCAGAGGAGTCTTTTGGAGATC 1446
Db 1875 GCTGGAAAGGATGAATATTCAGATGGGTGATTTGCCTCTCAGAGAAGTCTCCTTGAGGTC 1934
Qy 1447 ATGGCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTGTTCTTTGTGTCAGTAGGCCCT 1506
Db 1935 ATGGCTGAATTTCCATCAGCAAAACCTCCAAATTTGGTGTCTTTTTCAGCAGTGTGCTCCT 1994
Qy 1507 CGCTTACCGCTCGATACCTATCTATCTCATCTCTCTCAAGTTTCTCCTCAAGAAAT 1566
Db 1995 CGCTCGAGCTAGATTTTATTCGATCTCTCATCTCCAAGAAATGGTGCCAAACAGAAAT 2054
Qy 1567 CATGTGACGTGCTTGTAGTATATGTTCAAGCCCTACCGGAAGGTTTCAACCGAGAGTG 1626
Db 2055 CATGTTACCTGTGATAGTACATGAGAAATGCCCAACCGAAGGATTCACAAAGAGTG 2114
Qy 1627 TGTTGCAATGATGATGAGCAGTGTCTCAGAA-----TAGCTGGGCT 1671
Db 2115 TGTTCAACATGGATGAAGAAATCTGTACCAATGGAGAAAAGCCAGGACTGCACTGGGCT 2174
Qy 1672 CCTATTTTGTTCGAAGCTCAAACTTCAAGTTACGAGTACGCCCTCAACTCCAATATC 1731
Db 2175 CCTATTTTGTAGGACCTCCAATTTAGACTCCCTTCTGATTAATAAGTGCCCTATAATC 2234
Qy 1732 ATGGTGGGACCTGGTACAGGTTAGCTCTTTTTCAGAGGATTTCTGCGAAGAAAGATGGCC 1791
Db 2235 ATGATTTGGTCTCGACACTGGATGGCTCTTTTTCAGAGGTTTCTTTCAGGAAAGATTAGCT 2294
Qy 1792 CTCAAGAAATGGTGTCAACTTGGCCCAAGAGTGTCTTTTTCGATGTAGGAATCGT 1851
Db 2295 CTGAAGAGAGGAGCTGAATCTCGGCCCTCTCAGTTTATTTCTTTGATGTCAGGAACCGT 2354

Qy 1852 AATATGAGCTTCATTTTATGAAGACGAACATAACAACCTTCGTGGAAACGAGGAGTCATTTG 1911
Db 2355 CAAATGGACTACATCTATGAAGACGAGTTGATGCTACTTCGTTAATACTGGCGACTTGAT 2414
Qy 1912 GAGCTAGTTATTGCCCCCTTTTTCAGCTGGAAGGGGAAAAGAGGAATATGTTCAACATAAGATG 1971
Db 2415 GAGCTCATTTTGGCTTCTCTCGAGAGGGACCCCAAGGAGTATGTACAAACATAAAATG 2474
Qy 1972 ATGGAGAAAGCAACCGGATGTATGGAATGTATGATATCAGGGGACGGTTATCTCTATGTGTGT 2031
Db 2475 ATGGAGAAAGCTTCAGAAATTTTGGAGCATGATATCAAGAGGAGCTTACATTTATGTGTGT 2534
Qy 2032 GGTGATGCAAGGGAATGCGCAGAGATGTCATCGCACGTTCGCATACCATTTGCCCAAGAA 2091
Db 2535 GGTGATGCCAAGGCAATGCGCAGGATGTACACCGGCCCTGCACACAATTTTTCGAAGAG 2594
Qy 2092 CAGGGACCATGGAATCATCTGCTGCCGAAGCTGCAGTAAAGAACTCCAAGTTGAAGAA 2151
Db 2595 CAGGGTCTCTCGATAGTTTCCAAGGCTGAGAGCATGTTAAAGAACTTACAAACTACTGGC 2654
Qy 2152 CGATATCTAAGAGATGTCGTGGTGATCGAATGT 2183
Db 2655 AGATATTTCCGCGCATGTATGGTGATGATATCT 2686

RESULT 10

US-10-429-949-18
; Sequence 18, Application US/10429949
; Publication No. US20040002105A1
; GENERAL INFORMATION:
; APPLICANT: DIXON, RICHARD A.
; APPLICANT: ACHNINE, LAHOUCINE
; APPLICANT: SUZUKI, HIDEYUKI
; APPLICANT: HE, XIAN-ZHI
; APPLICANT: WANG, LIANGJIANG
; TITLE OF INVENTION: METHODS OF IDENTIFYING GENES FOR THE MANIPULATION OF
; FILE OF INVENTION: TRITERPENE SAPONINS
; FILE REFERENCE: NBL00202US
; CURRENT APPLICATION NUMBER: US/10/429,949
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/380,159
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 2581
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
US-10-429-949-18

Query Match 32.0%; Score 849; DB 17; Length 2581;
Best Local Similarity 65.3%; Pred. No. 8.7e-211;
Matches 1299; Conservative 2; Mismatches 667; Indels 21; Gaps 3;

Qy 203 TTTTCATTAATGTCACAACTGATGTTCAATGCTGATTCGATTTGTTCTTCGCAATGTA 262
Db 228 TTATGATCTTAACAACCTTCAATAGCTGTTCTCATCGGTTGCGTCTGTTTAAATTTGGC 287
Qy 263 TGAATCTTTCGTTCTTCTCAATCAAAACCTTATGAAACTTATAAACCAATAATTGATAAG 322
Db 288 GTAGATCCAATTTCTCAAAAACCAAAACCAATTTGAAGTCTTAACCGGTTATTCGAGA--- 344
Qy 323 AAGAAGAGAGAGATGGAAGTTGATCTCTGGTAAATTAAGCTCACTATATTTTTTGGTACTC 382
Db 345 AACTTCTTGAACCTTGAATCGATGCGGTACCAAAAAGTTACCGTTTCTTTTGGCAGTC 404
Qy 383 AGACTGGTACTGCTGAAGGATTTGCTAAGGCATTTGCGAAGAAATTAAGGCAAGTACA 442
Db 405 AAACCGGTACCGCGAAGGTTTTCGCAAGGCGATAGCGGAAGGCAAAAGCGCGTTATG 464


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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1764)
; OTHER INFORMATION:
US-10-188-523B-13

Query Match      30.5%; Score 807.6; DB 16; Length 1863;
Best Local Similarity 67.2%; Pred. No. 4.9e-200;
Matches 1197; Conservative 0; Mismatches 559; Indels 24; Gaps 3;

QY 415 TTGGCAGAAGAAATTAAGGCAAAAGTACAAGAAAGCAGTTGCTTAAAGTAGTTGACCTGGAT 474
DB 1 TTGTTGAAGAACGGAAGCGCGATATGAAGAGCTGTGTTTAAAGTGGTTGATTTGGAT 60
QY 475 GACTATGCCAGCCGAGGATGATCAATATGAAGAGAAATTAAGAAAGAGAGTCTTTTGGTGT 534
DB 61 GATTATGCTGCTGATGATGAGGAGTATGCAGAGAAATTCAGAAAGGAGACATTTGCTTTC 120
QY 535 TTCAATGGTAGCCACTTATGTTGATGTGAGCAACTGACAACTGCTCGGAGATTTTCAAA 594
DB 121 TTCTTCTTGCTACATATGAGATGTGAGCCAACTGATAATGCTGCAAGATTTTATAAA 180
QY 595 TGCTTCACTCAGGAACAATGAAGGGGAGAGTGGCTTCAGCAACTAACTTATGTTGTTTT 654
DB 181 TGCTTCAACCGAGGAGATGATAAGAGATTGCTTGAAGAACTTCACTATGTTGTTTT 240
QY 655 GGTTCGGTAAACCGTCAATACGAGCAATTCACAAGATCCGGTAGATGTGGATGAGCAA 714
DB 241 GGTCTTGGCAACAACAGATGAGCATTTCAACAAGATTGCATTAGTGGTTGATGAGGT 300
QY 715 CTCGGTAAACAAGGTGCNAAGCCATGTTCAAGTGGGCTCGTGACAGTATCAATGC 774
DB 301 CTCACAGAGCAGGTGCAAGCCCTTGTTCAGATTGGCTTGGAGATGACGATCAATCA 360
QY 775 ATTGAAGATGATTTTACTGCTGCGCAGAAATGCTGTGGACTCAATTGGATCAGTTGCTC 834
DB 361 ATTGAAGATGATTTTCTGCATGGAAGAAATAGTGTGGCTGAAATGGATCAATTTGCTT 420
QY 835 AAAGATGAGGATGCTGCTCTCAGTGGCTPACACCGTATATTGCTACTGTTCTCTGAATAC 894
DB 421 CTTGATGAAGACCAACAAGACT--GCTGCCACTCCTTACACAGCTGCCATTCCCGAATAC 477
QY 895 AGGGTAGTATTCACGAACACTACGTCGGCTCTGGATGATATAACACATAATCTGCT 954
DB 478 CGAGTCGTGTTTATGACAAACCTGATACGCTTTCCGAGAACTCA-----TAGTCAAACT 531
QY 955 AACGGGATGTTGCAATTTGATATTTCTCCATCTTCAGAAACCAATTTGTTGCTCAACAAGA 1014
DB 532 AATGGTCACTACTGTTCAAGATGCTCAACATCCATGCAATCCAAACGTGGCTGTTAAAAA 591
QY 1015 GAGCTCACAAACCCAGTCTGATAGATCTCTGATACATCTGAGTTCGACATATCAGGC 1074
DB 592 GAGCTCCATACCCCTGAATCCGATCGCTCTGCACTCATCTTGAATTTGACATCTCTCAC 651
QY 1075 TCTTCCCTTACATATGAGCTGAGATCATGTTGGTGTGTTATGCTCAGAACTCGGATGA 1134
DB 652 ACTGAGTATATACGAAACTGGGATCAGTCGGTGTCTACTGTGAAACCTTAATTGAA 711
QY 1135 ACTGTCGAGGAAGCAGGAAGCTGTTGGGTCAACCCCTGGATTGCTGTTTCAATTCAC 1194
DB 712 GTAGTGGAGGAAGCTGAGAAACTGATAGATTACAGAGATACTTATTTTCATTATACAC 771
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DB 772 ATTGATAAACGAAGATGGAACACCACTCGGTGGACCTACATGTCAGCTCTCTTCCCTCC 831
QY 1255 TGCACCTTAGCATCTGCCCTAGCACGCTATGCTGATCTTTTGAATCCTCTAGAAAGGCT 1314
DB 832 TGCATTTTAAAGAAAGATGACCAATACGAGATCTGTTGAGTGTCTCCCAAAAGTCA 891
QY 1315 TCTCTGATTTGCTGTCCGCTCATGATCTGTATCCAGTGAAGCAGAGATTCGCTTT 1374
DB 892 ACCTTGCTTGTCTAGTCGGCATGCTTCTGATGCCACTGAAGCTGATCGACTACAATTT 951
```

RESULT 13

US-10-341-961A-241

; Sequence 241, Application US/10341961A

; Publication No. US20040006787A1

; GENERAL INFORMATION:

; APPLICANT: Boyce Thompson Institute for Plant Research, Inc.

; APPLICANT: Curagen Corporation

; APPLICANT: Crasta, Oswald

; APPLICANT: Swirsky, Peter

; APPLICANT: Mysore, Kiran

; APPLICANT: Folkerts, Otto

; APPLICANT: Martin, Gregory

; APPLICANT: Ekengren, Sophia

; TITLE OF INVENTION: PLANT DEFENSE-RELATED GENES REGULATED IN RESPONSE TO PLANT-PATHOGE

; TITLE OF INVENTION: INTERACTIONS AND METHODS OF USE

FILE REFERENCE: BTI.67A2
 CURRENT APPLICATION NUMBER: US/10/341,961A
 CURRENT FILING DATE: 2003-01-14
 PRIOR APPLICATION NUMBER: 60390249
 PRIOR FILING DATE: 2002-06-20
 PRIOR APPLICATION NUMBER: 60261029
 PRIOR FILING DATE: 2001-01-11
 PRIOR APPLICATION NUMBER: 60348792
 PRIOR FILING DATE: 2002-01-14
 NUMBER OF SEQ ID NOS: 395
 SOFTWARE: Patencin version 3.1
 SEQ ID NO 241
 LENGTH: 1985
 TYPE: DNA
 ORGANISM: Lycopersicon esculentum
 US-10-341-961A-241

Query Match 29.1%; Score 770.2; DB 17; Length 1985;
 Best Local Similarity 68.0%; Pred. No. 3.1e-190;
 Matches 1126; Conservative 0; Mismatches 508; Indels 21; Gaps 3;

QY	542	TAGCCATTATGCTGATGCTGAGCCCACTGACAACTGACAACTGCTGCGAGATTTTACAAATGCTTCA	601
DB	3	TGGCAACATATGAGATGCTGGAACCACTGATATGCTGCCAGATTTCTATAAATGCTTTG	62
QY	602	CTCAGGAACATGAAGGGGAGAGTGGCTTCAGCAACTAACTTATGCTGTTTTGTTGG	661
DB	63	AAGAGGGGAAGAGAGGGTGACTGCTTAAAGAACTTCGTAAGAGATTTTGGGCTTG	122
QY	662	GTAAACCGTCAATACGAGCAATTTCAACAAGATCGCGTAGATGCGATGAGCAACTCGGTA	721
DB	123	GCAACAGACAATACGAGCAATTTTAAACAAGATTCCTAAAGTTGTCGATGAGCTTCTGCTG	182
QY	722	AACAAGGTGCAAGCGCATTTGTTCAAGTGGGGCTCGGTGAGATGATCAATGCAATTTGAAG	781
DB	183	AGCAAGGTGGCGAGAGGCTTTGTTCCAGTGGGCTTGGAGATGATGATCAATGCAATTTGAAG	242
QY	782	ATGATTTTACTGCTGCGGAGAAATTTGTTGGACTGAATTTGGATCAGTTGCTCAAAAGATG	841
DB	243	ATGATTTTGTGATGCTGAGTGGGAGTAGTGTGGCTGAAATAGATAGTTGCTTCTTGAGC	302
QY	842	AGGATGCTGCTCTCAGTGGCTACACCGPATATGCTACTGTTCTGTAATACAGGGTAG	901
DB	303	GGGATGATGCAACT--GCTACAACTCCATATACTGCTGCTGTTTGGGAATATAGGGTTG	359
QY	902	TGATTCAGCAACTACGGTGGCGCTCTGGATGATTAACACATAAA--TACTGCTAACG	958
DB	360	TTACCTATGCAAACTCCAACTTTTGTATGACGACTTGAACCAACAAATGGTCAATGCAAAATG	419
QY	959	GCATGTTGCAATTTGATATTTCTCCATCTTGCAGAACCAATGTTGCTCAACAAAGAGAGC	1018
DB	420	GACATGTCATGTTGATGCTCAACATCTCTGTCAGAGCTAATGTTGCTGTGAGGAAGAGC	479
QY	1019	TCACAAACCCAACTCTGATAGATCTCTGTATACATCTGGAGTTTCGACATATCAGGCTCTT	1078
DB	480	TTCATACTCCAGCTTCTGATCGTTCTTGCACTCATCTGGAGTTTGACATTTCTTGCACTG	539
QY	1079	CCCTTACATATGAGATGAGATCATGTTGGTGTATGCTGAGAACTCGGATGAACTG	1138
DB	540	GACTTACGTACGAACCTGGTGATCATGTTGGTGTGACTGTGAAAAATTTTGTGAAACCG	599
QY	1139	TCGAGGAAGCAGGGAAGCTGTTGGGTCAACCCCTGGATTTGCTGTTTCAATTTTCAACCG	1198
DB	600	TGAGAGAGCTGAAGAGCTACTGAATATATACCGGATATCTTTTTCATTTCAACACCG	659
QY	1199	ATAAAGAAGCAGGCTCAACCCAGGGAAGCTCAATACCACTCTCTTTCCAGAGTCTTTGCA	1258
DB	660	ATAAAGAGGATGSCACACCACTTTGGTGAAGTTTCAATGCACTCTCCATTTCCCTCTTGA	719
QY	1259	CCTTACATCTGCCCTAGCAGCGTATGCTGATCTTTTGAATCTCTCTAGAAAGGCTTCTC	1318
DB	720	CTTTTGAAACAGCATTTGACTCGGTATGCTGATGTTTGTGATTTCTCTCTCTCTCTCTCTT	779

QY	1319	TGATTTGCTCTGTCGCTCATGCTATGTTACCAAGTGAAGCAGAGAGATTTGCGCTTTTGT	1378
DB	780	TACTTGTCTTTAGGGGATGTTCTTCTGATCCAAATGAAGCTGATCATTAAGATATCTAG	839
QY	1379	CATCACTCTGGGAAAGAAATGAGTATTTCAAAATGGGTAGTTGGAAGTCAAGAGAGTCTTT	1438
DB	840	CATCACTCTGCGAAAGGAAGAAATATGCTCAGTGGATAGTTGCAAGTCAAGAGAGCTTTC	899
QY	1439	TGGAGATCATGGCCGAGTTTCCATCAGCAAAACCCCTCTTGGTGTGTTCTTTGCTGCGAG	1498
DB	900	TTGAAGTCAATGCTGAATTTTCTTTCAGCAAGCTTCAATCGGTGTTTCTTTGCTTCTG	959
QY	1499	TAGCCCTCTGCTTACCGCTCGATATTTCTATCTCATCTCTCTCTCAAGTTTGGCTCCCT	1558
DB	960	TTGCTCTCTGCTTACCAACCAAGATTTCTACTCCATCTCATCACTCTCTAGATGCGGCGAT	1019
QY	1559	CAAGAATCATGTGACGTGTGTTTATAGTATATGTTCAAAAGCCCTACCGAAGGTTTCAAC	1618
DB	1020	CTAGAATTCATGCTCACTTGTGCACTGTTTACGACAAATGCGCACTGGAGCAATTCACA	1079
QY	1619	GAGGATGTTGCGACATGATGAGCATGCGAGTCTCTCAGG-----TA	1663
DB	1080	AGGGTCTCTGCTCAACATGGAAGATGCTATTTCTCTAGAAGAAAGCTTTTCTCTGCA	1139
QY	1664	GCTGGGCTCTTATTTTGTTCGAACTCAAACTTCAAGTTTACAGCTGACCCCTCAACTC	1723
DB	1140	GTACGGCACTATTTTGTTCGCAATCAAACTTTAACTGCGAGCTGATTAACAGGTTTC	1199
QY	1724	CAATTATCATGTGGGACCTGTGTACAGGTAGTCTCTTTTACAGAGATTTTCTCAGGAA	1783
DB	1200	CAATCAATATGATTTGGCTGTGCTGATTTGTCACCACTTCAAGGTTTCTCAGGAA	1259
QY	1784	GAATGGCCCTCAAGGAAATGTTGCTCACTTGGCCAGCAGTCTCTTTTTCGGATGTA	1843
DB	1260	GAATGGCTTTGAAGGAGGAGGAGTGAACCTTGGTCTCTGAGTGTATTTTGGATGCA	1319
QY	1844	GGAATCGTAAATATGAGCTTCAATTTATGAAGACGAACCTAAACAACTTCTGTTGGAACGAGGAG	1903
DB	1320	GGACCGCCAAATGACATCACTATCAGATGAGTTAGATTAATTTCTTGGCCGGTG	1379
QY	1904	TCATTTGGAGTGTATTTTGTGCTTTTACGTGGAAGGGGAAAGAGGAATATGTTCAAC	1963
DB	1380	CACCTTCTAATCTAGTTTGTGCTTCTCAGTGAAGGACCTAAACAAAGAAATATGTCAC	1439
QY	1964	ATAAGATGATGAGAAAGCAACGATGATGATGATGATGATGATGATGATGATGATGATGAT	2023
DB	1440	ATAAATGACAGAGAGGCGGACGACATCTGGAACATGATTTCTCAGGAGGTTATGTTT	1499
QY	2024	ATGTGTGCTGATGCGCAAGGGAATGGCCAGAGATGCTCATGCGCTTGCATACCAATG	2083
DB	1500	ATGTGTGCTGATGCTTAAGGCGATGGCCAGGAGTGTCCATCGGACCTTTCACACTATTG	1559
QY	2084	CCCAAGAACAGGAGCCCATGGAATCATCTGTGCGAAGCTGCGAGTAAAGAACTCCAAG	2143
DB	1560	CTCAGGATCAGGAGTCACTTGTATGATCTTCAAGGCGCAGAGCTTTGTGAAGAAATTTG	1619
QY	2144	TTGAAGACGATATCTTAAGAGATGCTGCTGATCG	2178
DB	1620	CGACCGGAAGATATCTGCGTGTATGTTGTTGAATTTG	1654

RESULT 14
 US-10-437-963-1516
 ; Sequence 1516, Application US/10437963
 ; Publication NO. US2004012343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 1516
 ; LENGTH: 2136
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_101375C.1
 US-10-437-963-1516

Query Match 28.4%; Score 751.6; DB 19; Length 2136;
 Best Local Similarity 64.6%; Pred. No. 2.4e-185;
 Matches 1211; Conservative 0; Mismatches 609; Indels 54; Gaps 4;

 QY 328 GAGGAGATTGAAGTTGATCCTGTAAATTAAGCTCACTATATTTTGGTACTCAGACT 387
 DB 199 GAGGAGCGCGCGCGCGGAGGAGGAGCGGCTCACCGTCTTCTTCGGCAGCAGACC 258
 QY 388 GGTACTGCTGAAGGATTTGCTAAGGCATTGGCAGAGAAATTAAGCAAGTACAGAAA 447
 DB 259 GGCACCGCGAGGGCTTCGCCAAGGCACCTCGCTGAGAGGCTAAGTCAAGATACGACAAG 318
 QY 448 GCAGTTGTTAAAGTAGTTGACCTGGATGACTATGACGCGGAGGATGATCAATATGAAGAG 507
 DB 319 GCGATATTCAAAGTTGTGGACTTTGGATGAGTATGCGATGCGGATGAGGAGTACGAGGAG 378
 QY 508 AAATTAAGAAAGACTCTTTGGTGTGTTTTCATGGTAGCCACTTATGGTGAATGGTAGCCA 567
 DB 379 AGATTCAAGAAAGAGAAGATATCGTTGTTCTTCGTTGCAACGCTACGAGATGGTGAACCG 438
 QY 568 ACTGACAAATGCTCGAGATTTTACAATGGTTTCACTCAGGAACATCAAAAGGGGAGAGTGS 627
 DB 439 ACTGACAAATGCTCGAGTCTAGTTCTATAAATGGTTCACTGAGGGAATGAGAGGGTGTGG 498
 QY 628 CTTTACAGCAACTAATCTATGGTGTGTTTGGTAAACCGTCAATACGAGCATTTCAAC 687
 DB 499 TTGAATGACTTCCAGTATGCTATTTTGGCTTGGCAATCGGCAGTATGAGCAATTTCAAC 558
 QY 688 AGATCGCGGTAGATGAGTAGCAACTCGGTAAACAAGGTCAAAAGCGCATTTGTTCAA 747
 DB 559 AAGGTTGCCAAGGTTGTGATGAGTCTTAGTTGAGCAAGGTTGGAACGCTCTGTGTCG 618
 QY 748 GTGGGCTCGGTGACGATGATCAATGCAATGGAAGATGATTTTACTGCTTGGCGAGAAATTG 807
 DB 619 GTTGGTCTTGGAGATGATGATCAATGCAATGAGATGACTTCAACGCATGGAAGAACT 678
 QY 808 TTGTGACATGAATTTGGATCAGTTGCTCAAAGATGAGGATGCTGCTCTTTCAGTGGCTACA 867
 DB 679 CTCTGCCAGAAATTGGATCAGTTACTTTCGGGATGAAATGATGTTTCAACAGGCACTA-- 736
 QY 868 CCGTATATTGCTACTGTTCTGTAATACAGGATGATTCACGAACACTACGCTCGCGCT 927
 DB 737 -CCTACACAGCTGCCATTCTGTAATACCGGTTGAAATTTGTTAAGCCTGATGAGGCGCC 795
 QY 928 CTGGATGATAAACAATTAATCTGCTAACCGGAGTGTTCATTTTGCATATTCTCCATCTCT 987
 DB 796 CATTTGGAGAAATTTCACTGCTTGCAACAGGTTATGCGGTTCAATGCTCAGCATCTCT 855
 QY 988 TGAGAACCAATTTGCTCAACAAAGAGAGCTCCACAAACCCCAAGTCTGATAGATCCTGT 1047
 DB 856 TGCCGGGCCCAACGCTGCTGTCGACGCGGAACCTCACACTCTGCTTCTGATCGTTTCATGC 915
 QY 1048 ATACATCTCGAGTTCCACATATCAGGCTCTTCCCTTACATATGAGACTGGAGTCAATGTT 1107
 DB 916 ACTCACTTGGAGTTTGACATGTTGTCGACCTGGTCTTACGATGTAACACCGGTGACCAATGTT 975
 QY 1108 GGTGTTTATGCTGAGAACTCGCATGAAACTGTGCGAGGAAGAGGAGCTGTTGGGTCAA 1167

DB 976 GGTGTATACACAGAGAACTGCCCTCGAGGTTGTAGAGGAGGACAGAGGTTGTTAGGCTAC 1035
 QY 1168 CCCCTGGATTTCGTGTTTTCATATTCACACGGAATAAAGAGAGCGGTCACCCC---AGGGA 1224
 DB 1036 TCCCCAGAGGCTTTTTCACCATCCATCGACAGCAAGAGACGGTACACCACTAGGTGGT 1095
 QY 1225 AGCTCATTTACACCTCTCTTCCAGGTCCTTCCAGCTTTCAGGATCTGCCCTAGCACCGCTAT 1284
 DB 1096 GGTCTCTGGCTCCTCCATTCCTCCCGATTACTGTGAGGAATCGCTTGTAGATAT 1155
 QY 1285 GCTGATCTTTTGAATCCTCTAGAAAGGCTTCTCTGATTGCTCTGCTCCGCTCATGCTAT 1344
 DB 1156 GGGATCTTCTGAAATTCGCCGAGAAAGAGTGTCTTGGTTGCATTAGCTACTTATGCTTCA 1215
 QY 1345 GTACCCAGTGAAGCAGAGAGATTGCGCTTTTGTTCATCACTCTGCGGAAGAAATGAGTAT 1404
 DB 1216 GATTCTACTGAAGCTGATCGTCTGAGGTTCTTGGGCTCTCTCTGCTGGAAGGATGAGTAT 1275
 QY 1405 TCAAAATGGGTAGTTGGAAGTCAAGGAGTCTTTTGGAGATCATGSCCGAGTTCATCA 1464
 DB 1276 GCTCAATGGGTTGTTTCGAGTCAAAAGAGTCTATTAGAAAGTGAATGCGCAGAGTTCCTTCA 1335
 QY 1465 GCAAAACCCCTCTTGGTGTGTTCTTCTGCTGAGTAGCCCTCGCTTACCGCTCGATAC 1524
 DB 1336 GCAAGCCTCCACTAGGAGTCTTCTTTCGAGCGCTTCTCTGCTTTCAGCGGAGATAC 1395
 QY 1525 TATTCTATCTCATCTCTCTTAAGTTTGTCTCAAGAAATTCATGTGACGTGTGCTTTA 1584
 DB 1396 TACTCAATTTCTCTTCACTAGTACCTGACCTACCCAGAAATTCATGTTACATGTGCACCT 1455
 QY 1585 GTATATGTTCAAAAGCCCTACCGAAGGTTTACCGAGGAGTGTTCGACATGGAAG 1644
 DB 1456 GTCCATGAAAAAACCTCTGCTGGAAGGTTACATAAGGAGTCTGCTCAACATGGATTAA 1515
 QY 1645 CATGCAAGTTTCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAACG 1689
 DB 1516 AATGCTATTCATCAGAGAGACAAAGGACTGACGCTGGGCTCCAGTTTGTGAGACAA 1575
 QY 1690 TCAAACTTCAAGTTTACAGCTGACCCCTCAACTTCAATTTATCATGGTGGGACTGTGTA 1749
 DB 1576 TCAAACTTCAAACTGCTGCTGATCTTTCAGTACCGGTTTATCATGATTGGCCAGGAAC 1635
 QY 1750 GGGTTAGCTCTTTCAGAGGATTTCTGCAAGGAAGAAATGCGCCTCAAGGAATGCTGCT 1809
 DB 1636 GGTCTGTCTCTTTCGCGGATTTCTTGCAGGAGAGGCTGCTCTCAAAAACAATCAGGAGCT 1695
 QY 1810 CAACTTGGCCAGCAGTGTCTTTTTTCGGATGTAGGAATCGTAATATGAGCTTCAATTTAT 1869
 DB 1696 GAGCTTGGTGGCTCGGTATTTCTTTCGATGCAAGAAACAGCAAGATGAGTTCATCTAT 1755
 QY 1870 GAAGACGAACATAACAACTTCTGGAACAGGAGTCAATTTTCGGAGCTAGTTATGCTTTT 1929
 DB 1756 GAGGATGAGCTGAACACTTCTTTCGGAAGGAGCATTTGTCGAGCTGTTCTCGCTTC 1815
 QY 1930 TCACTGTGAAGGGAAGAGGAATATGTTTCAACATAAGATGATGAGAAA----- 1980
 DB 1816 TCTCGTGAAGGCGCTTACGAAGGAATACGTGACAGCAAAATGTGCGAGAAAGCTTGCTCA 1875
 QY 1981 -----GCAACGATGTATGGAATGTGATATCAGGGGACGGT 2016
 DB 1876 TATTTCTTACCTTTGTCTGTCAGGCTTCCGAAATCTGGGACATGATCTCCAGGGTGGT 1935
 QY 2017 TATCTCTATGTGTGTGATGTCGAAGGAAATGGCCAGAGATGTCATCGCAGGTGCAAT 2076
 DB 1936 TACATTTACGCTGTGTGTGATGTCGAAGGATGCGCCAGAGATGTACATAGAGTTCTCCAC 1995
 QY 2077 ACCATTTGCCAAGAACAGGACCCCAATGGAATCATCTGCTGCCGAAGCTCGACGATAAGAAA 2136
 DB 1996 ACATTTGTACAGAACAGGATCACTTGACAGCTCTAAGGCTTGAGAGCTTTGTGAAGAGC 2055
 QY 2137 CTCCAAGTTGAAGA 2150
 DB 2056 CTCCAAACGAGGA 2069

RESULT 15

US-10-425-115-99832
; Sequence 99832, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 99832
; LENGTH: 2149
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_22561C.1
US-10-425-115-99832

Query Match 28.3%; Score 750.8; DB 20; Length 2149;
Best Local Similarity 66.0%; Pred. No. 3.9e-185;
Matches 1142; Conservative 0; Mismatches 567; Indels 21; Gaps 3;

QY	464	TTGACCTGGATGACTGACGCGAGGATGATCAATATGAGAGAAATTAAGAAAGAGT	523
DB	19	TGGTCGGGTTGCTTCTGCTGCGGACCCGCGCTGCGGAGGAGGTGTAGGCCAGT	78
QY	524	CTTTGGTGTTCATGGTAGCCACTTATGGTGTATGGTAGGCACTGACATGCTGCGA	593
DB	79	GGCTAGCGTGTCTTCTGCGGCAACGATGAGATGGTAGGCGGACTGCAATGCTGCTA	138
QY	584	GATTTTACAAATGGTTCACTCAGAACATCAAGAGGAGAGTGGCTTCAGCACTAACTT	643
DB	139	GGTTCTACAAATGGTTCACTCAGGGAATGAGAGGAGTGTGCTGCTAAATGACTTTGAGT	198
QY	644	ATCGTGTGTTTGGTGGTAAACCGTCAATACGAGCATTTCAACAAGATGCGGATAGTG	703
DB	199	ATGCTGTGTTTGGTCTGGGCAACCGCAGTATGAGCATTTCAACAAGTTGCCAAGTAG	258
QY	704	TGATGAGCAACTCGGTAAACAGGTGCAAGGCGCAATGTTCAAGTGGGGCTCGGTGACG	763
DB	259	TCGATGAGATTCCTGACAGAACAAAGGTGGAAAGCGCCTTGTTCAGTTGGTCTTGGGGACG	318
QY	764	ATGATCAATGCTATGAAGATGATTTTACTGCTTGGCGAGAAATGTTGTGGACTGAATTTGG	823
DB	319	ATGACCAATGCAATGAGATGACTTCAATGCAATGGAAGAGCTCTCTGGCCAGAGTTGG	378
QY	824	ATCAGTTGCTCAAGATGAGGATGCTGCTCTTTCAGTGGCTACACCGTATATGCTACTG	883
DB	379	ATCGATTACTTCGGGATGAAATGATGCTCTCCAGGCCCTACA---TACACAGCTGCAA	435
QY	884	TTCTGTAATACAGGTAGTGAATTCACGAACTAGGTGCGGGCTCTGGATGATAACACA	943
DB	436	TTCTGTAATACAGGTAGTGAATTCATCAAACTGAGGAGGAGCTCAATTTGGAGAGAACT	495
QY	944	TAAATACTGCTAACCGGAGTGTTCATTTGATATTTCTCCATCTTCGAGAACCAATTTGG	1003
DB	496	TCAGCTTTGCAATGGCCATGCAATGATGATGATGATGATGATGATGATGATGATGATG	555
QY	1004	CTCAACAAAGAGAGCTCCCAAAACCAAGCTGATAGATCTGATATATATCTGAGTTGCG	1063
DB	556	TCGTGCGGAGGAACCTCCACCCCTGCTTCTGATGATGATGATGATGATGATGATGATG	615
QY	1064	ACATATCAGGCTCTTCCCTTACATATATGATGATGATGATGATGATGATGATGATGATG	1123
DB	616	ACATTGCTGCACTGCTCAGCTATGAAACTGGCGACCATGTTGGTGTATATACACCGAGA	675

QY	1124	ACTGCGATGAAACTGTCGAGGAGCAGGAGAGCTGTTGGTCAACCCCTGGATTGCTGT	1183
DB	676	ACTGCGCTGAGGTTGTAGAGAGGCGAGAGAGTGTGTTGGCTACTCGCCAGACACATTTT	735
QY	1184	TTTCAATTCACACGGGATAAAGAGACGG---GTACCCCGAGGGAAGCTCATTTACCACCTC	1240
DB	736	TCACCATCCATGCAGACAAAGAGAGATGGCACCTTCACTAAGTGGCAGTCTCTTGTCTCTC	795
QY	1241	CTTTCCCGAGTCTCTGACCTTACGATCTGCCCTAGCAGCTATGCTGATCTTTTGAATC	1300
DB	796	CGTTCCCTCCCAATCAAGTGAAGATGCACTTCTAGATATGCGGACCTTTCTAAAT	855
QY	1301	CTCCTAGAAAGGCTTCTCTGATTGCTCTGCTCGCTCATGCTGATACCCAGTGAAGCAG	1360
DB	856	CACCGAAGAGGCTTCTCTGGTTGCATTAGCTTCTTATGCTTCAGATCTCTGCTGAGGCTG	915
QY	1361	AGAGATTGCGCTTTTGTCTATCACTCTCGGAAAGAAATGATATCAAAATGGGTAGTTG	1420
DB	916	ATCGTCTGAGGTTCTTGGCTCTGCTGCTGGCAAGGATGATGATGCCAATGGGTTGTGG	975
QY	1421	GAAGTCAGAGGAGTCTTTTGGAGATCATGCGGAGTTTCCATCAGCAAAACCCCTCTTG	1480
DB	976	CAAGTCAGAGAGGCTGTTGGAAGTATGCGAGAGTTCCCTTCGGCAAGCCCTCCACTAG	1035
QY	1481	GTGTGTTCTTTGCTGAGTAGCCCTCGCTTACCGCTCGATACTATTCTATCTCATCTT	1540
DB	1036	GAGTCTTCTTTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	1095
QY	1541	CTCCTAAGTTTGTCTCCTCAAGAAATTCATGTGACGTGTCTTTAGTATATGTTCAAGCC	1600
DB	1096	CACCTAGTATGGCAACCAACAGGATTCATGTACATGTGCTGCTGCTGCTGCTGCTGCTG	1155
QY	1601	CTACCGAAGGCTTACCGAGAGTGTGTCGACATGATGATGATGATGATGATGATGATGATG	1660
DB	1156	CGCTGGAAGGGTACATAAGGGAGTTTGTCTCACTTGGATTAAGATGCTGTTCTCTCGG	1315
QY	1661	A-----TAGCTGGCTCTCTATTTTGTTCGAAAGCTCAAACTTCAAGTTAC	1705
DB	1216	AGGAGAGCAAGGATGCGAGCTGGCTCCGATATTTGTGAGGCAATCAAACTTCAAACTAC	1275
QY	1706	CAGCTGACCCCTCAACTCCAAATTCATGTTGGGACCTGGTACAGGGTTAGCTCTTTTCA	1765
DB	1276	CGCTGATCTTTCAGTACCGATTCATGATTTGGCTGGGACCGGTCTTGCAACCCCTTCC	1335
QY	1766	GAGGATTTCTGAGGAAAGAAATGGCCCTCAAGGAAATGGTGTCTCACTTGGCCAGCAG	1825
DB	1336	GTGGCTTCTTGGAGGAAAGACTTGTCTCAAAAGAAATCTGGAGCTGAGCTTGGTCTGATCTG	1395
QY	1826	TGCTCTTTTTCGATGTAGGAATCGTAATATGAGACTTCAATTTATGAAGACGAACTAAACA	1885
DB	1396	TGTTCTTCTTGGATGCAAGAACAGCAAGATGAGCTTCACTATGAGGGGAGCTGACACA	1455
QY	1886	ACTTGTGGAACGAGAGTCAATTCGAGCTAGTTATTCGCTTTTTCACGTGAAGGGGAAA	1945
DB	1456	ATTTGTGAGCAAGGAGCACTGTCTGAGCTGGTCTTCTGCTTCTCGCCAGGCGCTTG	1515
QY	1946	AGAGGAATCTTCAACATAGATGATGAGGAAAGCAACGATGATGATGATGATGATGATGAT	2005
DB	1516	CTAAGGAATATGTGAGCAACAAATGGCAAGAAAGCATCTGAAATCTGGGACATGATCT	1575
QY	2006	CAGGGGACGGTTATCTCTATGTGTGTGTGATGCGCAAGGGAATGGCCAGAGATGTCATC	2065
DB	1576	CCCAAGGTGCTTACATCTATGTCTGTGTGACGCGCAAGGCAATGGCCAGAGAGTACATA	1635
QY	2066	GCAGTTGCAATACCAATGTCGCAAGAACAGGACCCCATGGAATCATCTGCTGCCAAGCTG	2125
DB	1636	GAGTTCTCATACCAATGTTTTCAGGAGCAGGGCTCTCTCGACAGCTTCTAAGGCGGAGCT	1695
QY	2126	CAGTAAAGAACTCCAAAGTTGAAGACGATATCTAAGAGATGCTCTGCTGA	2175
DB	1696	TCGTGAAGAACTCCAAATGGAGGGGAGATATCTTGAGGATGTGTGTTAA	1745

Search completed: October 19, 2005, 16:45:29
Job time : 5870 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:01:55 ; Search time 8887 Seconds
(without alignments)
12168.363 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
Sequence: 1 cggcagcagctgttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 45554873 seqs, 20411521753 residues
Total number of hits satisfying chosen parameters: 91109742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_Main:*

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2:	/cgn2_6/ptodata/1/pna/PCTUS2_COMB.seq.*
3:	/cgn2_6/ptodata/1/pna/PCTUS3_COMB.seq.*
4:	/cgn2_6/ptodata/1/pna/PCTUS4_COMB.seq.*
5:	/cgn2_6/ptodata/1/pna/PCTUS5_COMB.seq.*
6:	/cgn2_6/ptodata/1/pna/PCTUS6_COMB.seq.*
7:	/cgn2_6/ptodata/1/pna/PCTUS7_COMB.seq.*
8:	/cgn2_6/ptodata/1/pna/PCTUS8_COMB.seq.*
9:	/cgn2_6/ptodata/1/pna/PCTUS9_COMB.seq.*
10:	/cgn2_6/ptodata/1/pna/PCTUS10_COMB.seq.*
11:	/cgn2_6/ptodata/1/pna/PCTUS11_COMB.seq.*
12:	/cgn2_6/ptodata/1/pna/PCTUS12_COMB.seq.*
13:	/cgn2_6/ptodata/1/pna/PCTUS13_COMB.seq.*
14:	/cgn2_6/ptodata/1/pna/PCTUS14_COMB.seq.*
15:	/cgn2_6/ptodata/1/pna/PCTUS15_COMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:01:52 ; Search time 12772 Seconds
(without alignments)
2923.857 Million cell updates/sec

Title: US-09-486-757-10
Perfect score: 2649
Sequence: 1 cggcagcagctttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 26893129 seqs, 7048604437 residues

Total number of hits satisfying chosen parameters: 53786258

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query
No.	Score Match Length DB ID

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:01:52 ; Search time 7650 Seconds

(without alignments)
13180.686 Million cell updates/sec

Title: US-09-486-757-10

Perfect score: 2649

Sequence: 1 cggcagcagctgttagtat.....ttttgagaaaaa 2649

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479087

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_hic:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gssi:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	978.8	36.9	2343	3	CNS0A2GR
2	875.8	33.1	2362	3	CNS0A2GR
3	640.2	24.2	1813	3	AY103952
4	460.8	17.4	1596	9	CL969868
5	433.4	16.4	876	6	CB976975
6	428.8	16.2	835	7	CO163167
7	426.4	16.1	893	7	CO254258
8	421	15.9	806	7	CO166163
9	419.2	15.8	907	7	CO084955
10	418.8	15.8	928	7	CK271587
11	415	15.7	855	7	CO368449
12	413.8	15.6	729	4	BM535223
13	413.6	15.6	690	5	BU813507
14	412.2	15.6	853	7	CNS49512
15	411	15.5	824	7	CO109078
16	405.6	15.3	763	4	B1923088
17	394.4	14.9	659	1	AI730999
18	394	14.9	775	2	BF003997
19	393.4	14.9	837	7	CN125396
20	387.8	14.6	793	7	CN189862
21	387.6	14.6	782	7	CNS20768
22	387	14.6	867	7	CF832302
23	383.8	14.5	837	7	CO368300
24	381.2	14.4	647	7	CF418771

25	380.2	14.4	846	6	CB670323
26	380	14.3	670	7	CF542988
27	380	14.3	857	6	CD438804
28	379.8	14.3	849	6	CA289299
29	379.6	14.3	843	7	CO199633
30	378.4	14.3	710	6	CA159247
31	378.2	14.3	659	2	AW695744
32	377.6	14.3	858	7	CF832300
33	371.4	14.0	658	2	AW236561
34	370.6	14.0	750	7	CO166517
35	369.2	13.9	848	7	CO132719
36	366.6	13.8	683	2	AW398515
37	366	13.8	767	6	CA158489
38	366	13.8	827	7	CO201857
39	365.2	13.8	777	6	CA157581
40	364	13.7	692	7	CO158240
41	361.2	13.6	599	6	CB007356
42	359.4	13.6	791	7	CO362574
43	358.6	13.5	705	6	CA099956
44	358	13.5	783	7	CF447166
45	357.6	13.5	824	4	EG319913

ALIGNMENTS

RESULT 1

CNS0A2GR

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

CNS0A2GR 2343 bp mRNA linear HTC 06-FEB-2004
Arabidopsis thaliana Full-length cDNA Complete sequence from clone
GSLTSL53ZF02 of adult vegetative tissue of strain col-0 of
Arabidopsis thaliana (thale cress).

EX827429

HTC; GSIT cDNA.

Arabidopsis thaliana (thale cress)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi

1 (bases 1 to 2343)

Castelli, V., Aury, J.M., Jaillon, O., Wincker, P., Clepet, C.,

Menard, G., Cruaud, C., Quetier, F., Scarpelli, C., Schachter, V.,

Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.

Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:

A Combined Approach to Evaluate and Improve Arabidopsis Genome

Annotation

Unpublished

2 (bases 1 to 2343)

Genoscope.

Direct Submission

Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

The sequences are based on single pass reads

Life Technologies (a division of Invitrogen) members carried out

full-length libraries construction : Temple G.

Genoscope members carried out sequencing and annotation : Castelli

V., Aury J.M., Jaillon O., Wincker P., Menard M., Cruaud C.,

Schachter V., Weissenbach J., Salanoubat M.

URG INRA : Clepet C., Caboche M.

Annotation is based on the June 2003 version of the Arabidopsis

genome released by MIPS (Munich Information center for Protein

Sequences). 5 prime and 3 prime are assembled with Phrap.

http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full

length

http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

Location/Qualifiers

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/mol_type="mRNA"

/strain="Col-0"

/db_xref="taxon:3702"

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Db	1717	ATGCTGTGCTTACGAGAAGAGTGAACCTGTTCTCGGGCGGATATTTGTAGGCAA	1776
Qy	1690	TCAAACCTCAAGTTACAGCTGACCCCTCACTCCAAATATATCATGTGGGACCTGGTACA	1749
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Qy	1750	GGGTAGCTCTTTTCAGAGATTTCTCGAGGAAGATGCCCTCAAGAAATGTGCT	1809
Db	1837	GGATTAGCTCCATCAGAGATTCCTTCAGAAAGACTAGCGTTGGTAGAATCTGTGTT	1896
Qy	1810	CAACTTGGCCAGCAGTCTCTTTTCGGATGTAGGAATCGTAAATAGGACTTCATTTAT	1869
Db	1897	GAACCTGGGCCCATCAGTTTGTCTTTGGATGACAGAAACGGTAGAATGGATCTCATCTAC	1956
Qy	1870	GAAGACGAATAAACAACCTTCGTGGAAACGAGGAGTCAATTTCCGAGCTAGTTATTCCTTT	1929
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Qy	1930	TCACGTGAAGGGGAAAGAGGAATATGTTCAACATAAGATGATGAGAAAGCAACGGAT	1989
Db	2017	TCTCGTGAAGGCCACCAAGAAATACGTACACCAAGATGATGACAAAGGCTTCTGAT	2076
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Db	2257	TGGTAAAGAA	2267
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DEFINITION	Zea mays	1813 bp	linear
ACCESSION	AY103952		
VERSION	AY103952.1	GI:21207030	
KEYWORDS	HTC.		
SOURCE	Zea mays		
ORGANISM	Zea mays		
REFERENCE			
AUTHORS	Hainey, C.F., Dolan, M., Miao, G.H., Vogel, J.M., Whittitt, M.S., Arthur, L.W., Hanafey, M., Morgante, M., and Tingey, S.V.		
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes		
JOURNAL	Unpublished (2002)		
REFERENCE	2 (bases 1 to 1813)		
AUTHORS	Coe, E.H.		
TITLE	Direct Submission		
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA		
COMMENT	If you are interested in getting corresponding physical clones, these are publicly available from ZmDB and may be found by BLAST searching at MSL, maizemap.org; ZmDB, www.zmdb.iastate.edu; TIGR, www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the maize cDNA sequences is either Virginia Walbot, Stanford or Pat Schnable, Iowa State, then clones may be requested from ZmDB: www.zmdb.iastate.edu.		

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	/db_xref="taxon:4577"	
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	/note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project"	
ORIGIN		
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	Best Local Similarity	68.1%; Pred. No. 4.4e-165;
	Matches	945; Conservative 0; Mismatches 418; Indels 24; Gaps 3;
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DB	11	GCAGAAATTTAGATCAATGCTCCGCGACGAGGATGACACAACTGGTGCATCGACTCCATA
QY	873	TATTGCTACTGTTCTGTAATACAGGATGATGATTCAGAAACTACGGTCCGGCTCTGGA
DB	71	TACTGCTGATTTCTCTGTAATACAGAGTTGTTTTCATTGACAAATCTGACCTGTCAATCCA
QY	933	TGATAAACAACATAAATACTGCTAAACGGCGATGTTGCAATTTGATATTTCTCCATCTCTGCAG
DB	131	AGATAGATCATGGAACACTAGCCAAACGTTACTGGTGTGATGATTTCAACACCTTGCAG
QY	993	AACCAATGTTGCTCAACAAAGAGAGCTCCAAACCCAAAGTCTGATAGATCTGTATACA
DB	191	GTCTAATGTTGCTGTTCCGGAAGAGCTGCACAAACAGCTTCAGATCGCTCTGTATCCA
QY	1053	TCGAGATTGCAATATCAGGCTCTTCCCTTACATATGAGACTGGAGATCATGTTGGTGT
DB	251	TCTCGAGTTTGACATTTCTGGCACTGGTCTTGTGTATGAACCGGAGACCATGTTGGTGT
QY	1113	TTATGCTGAGAACTGCGATGAAACTGTGAGGAAGCAGGGAAGCTGTGGGTCAACCCCT
DB	311	ATATGAGAAATTTCTGTTACACTGTGAGAGAGTTGAAAGGCTACTTGAACCTTCTCC
QY	1173	GGATTTGCTGTTTCAATTCACACGATGAAAGACGGGTCAACCC-----AGGGAAG
DB	371	AGACACATTTCTTCCATCCATGCAGATGCAGAAAGATGGATCTCTCTGTAAGAGGAGG
QY	1227	CTCATTTACACCTCTTTCAGGCTCTTGCACCTTACGATCTGCCCTAGCAGCTATGC
DB	431	TTCTTGGCCCCACCTTTCCCATCTCCATGTACCTTGGGACTGGCGTTCTAGGATATGC
QY	1287	TGATCTTTTGAATCTCTCTAGAAAGGCTTCTCTGATTTGCTCTGCTCGCTCATGCACTGT
DB	491	TGATCTCTCATTCACACCGAAGAGGCTGCTTGTGCTTTTGTGCTTCTCATGCACTGA
QY	1347	ACCAAGTGAAGCAGAGAGATGCGCTTTTGTGATCATCCTCTGGGAAAGATGAGTATTC
DB	551	TCCAGCTGAAGCTGAACGACTTAGGTCTTGGCCTCTCTCTGTTGGAAGGATGAGTATTC
QY	1407	AAATGGGTAGTTGGAGTGCAGAGGATCTTTTGGAGATCATGGCCGAGTTCATCAGC
DB	611	TCAATGGATAACTGTGTAGTCAGAGGAGTCTTCTTGAAGTTATGGCCGCAATCCCTT
QY	1467	AAACCCCTCTTGTGTTGTTCTTGTGCTGAGTAGCCCTCGCTTACCCTCGATACATA
DB	671	TGAGCCACCATCGGAGTGTGTTTGTGCAATAGTCTCTCTGCTGCAACACGATACATA
QY	1527	TTCTATCTCATCTCTCTCTTAA---GTTTCTCTCTCAAGAAATCATGTCAGCTGCTTT
DB	731	CTCAATTTTCATCTCTCCAAACAGGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
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851 GAATACAAATTCCTCTGGAATATAGCGAAGATGAGCTGGCTCCCATATTTTGAGGCA 910
1689 GTCAAACTTCAAGTTACAGCTGACCCCTCAACTCCAAATTCATGTGGGACTGTGAC 1748
911 GTCAATTTCAAGTTACCTGCTGATCTGTCTCACTCCGATTCATGATGTTGCTCTGAGAC 970
1749 AGGTTAGCTCCTTTACAGAGATTTCTGCAGGAAGAAATGCCCTCAAGGAAAATGTGC 1808
971 AGGCTGGCTCCTTTTAGAGGCTTCTTGACGAAAGGTTAGCATTTGAAACAACTCGGAGC 1030
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RESULT 4

CL969868
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DEFINITION
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FEATURES

source

Location/Qualifiers

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Best Local Similarity 66.9%; Pred. No. 1.7e-115;
Matches 673; Conservative 0; Mismatches 327; Indels 6; Gaps 1;
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QY 460 GTAGTTGACCTGGATGACTATGCAGCCGAGGATGATCAATATGAAGAGAAATTAAGAAA 519
DB 208 GTTGTGATCTGGATGACTATGCAGCTGAGGATGAGGAGTACGAGGAGAGCTCAGGAAG 267
QY 520 GAGTCTTTGGTGTTCATGTGTAGCCACTTATGTGTAGTGTGTAGTGTAGTGTGTAGTGTGT 579
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QY 580 GCGAGATTTTACAAATGTTTCACTCAGGAACATGAAGGGGAGAGTGGCTTTCAGCAACTA 639
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DB 388 AAGTATGCTGTTTGGCTGGGAAATAGGCAGTATGAGCAGTTTAAAGGTTGCAAG 447
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DB 508 GAT 567
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DB 568 TTGGACCAACTGCTCGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 627
QY 880 ACTGTTCTGATACAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 939
DB 628 GCTATACCTGAATACAGAAATTTGATTTATTTGATTAATTCAGATGATGATGATGATGAT 687
QY 940 CACATAAATGCTTAACGCGGATGTTGATTTGATTTGATTTGATTTGATTTGATTTGATTTG 999
DB 688 TCGTGTCTCTGCTCAATGCGAGTGTGTTATTTGATTTTACCATCTCTGTGAGTCTAAT 747
QY 1000 GTTGTCTCAAAGAGAGCTCCAAACCAAGCTCTGATAGATCTCTGATACATCTGGAG 1059
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QY 1234 CACCTCTCTTTCAGGCTCTTGCACCTTACGATCTGCGCTAGCAGCTGCTGCTGCTGCT 1293
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1108 GAAGCTGAAGATGAGATTTTGGCTTCCCTCTCGGAAGGATG 1153

RESULT 5
CB976975 876 bp mRNA linear EST 01-MAY-2003
LOCUS CAB40003_Ila_Fa_B09 Cabernet Sauvignon Berry - CAB4 Vitis vinifera
DEFINITION cDNA clone CAB40003_Ila_Fa_B09 5', mRNA sequence.
ACCESSION CB976975
VERSION CB976975.1 GI:30300181
KEYWORDS EST.
SOURCE Vitis vinifera
ORGANISM Vitis vinifera
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; Vitaceae; Vitis.
REFERENCE 1 (bases 1 to 876)
AUTHORS Goes da Silva,F., Iandolino,A., Lim,H., Baek,J., Leelie,A., Xu,J.,
Jones,K. and Cook,D.
Expressed sequence tags from Vitis vinifera 'Cabernet sauvignon'
berries at various developmental stages
Unpublished (2003)
Contact: Douglas Cook, PhD
CAES Genome Facility
UC Davis, Plant Pathology
One Shields Ave, Davis, CA 95616, USA
Tel: 530 754 6561
Fax: 530 754 6617
Email: drcook@ucdavis.edu
Seq primer: ACGGTACCGACATATGCC.
FEATURES
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            'Cabernet Sauvignon'. Clone 8 berries. Sampled berries were
            collected from field-grown vines during stage II of berry
            growth (berries were green and hard) at approximately 60
            days after full bloom.The average berry size was 9
            millimeters. Sampled vines were located at the University
            of California, Davis, Experimental Vineyard. cDNAs were
            made by oligo-dT priming and directionally cloned. 5' and
            3' adaptors were used in cloning as follows:
            5'-AACGATGGTATCAAGCAGAGTGGCCATACGCCGGG-3' and
            5'-ATTCTAGAGCCGAGCGGCACATG-dT(30)NN-3'. Library was
            constructed using the Clontech Creator SMART kit and
            size-selected to contain the 0.5-3 kb size fraction."

ORIGIN
Query Match 16.4%; Score 433.4; DB 6; Length 876;
Best Local Similarity 71.2%; Pred. No. 5.4e-108;
Matches 623; Conservative 0; Mismatches 231; Indels 21; Gaps 3;

QY 1040 GATCCTGTATACATCTGGAGTTTCGACATATCAGGCTCTTCCCTTACATATGAGACTGGAG 1099
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QY 1100 ATCATGTTGGTGTATGTGACAACTGCGCATGAAACTGTCCAGGAGGAGGAAAGCTGT 1159
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Db 61 ATCATGTTGGTGTGTACTGTGAGAACTCCCTGAACACAGTGGAGGAGGCTGAAAGGTTGT 120
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238 CTCGGTATCGAGATGTTTGTAGTTCTCCCAAAAAGTCTGCTTTGGTTGCTCTAGCCGCC 297
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358 ATGAATATGCACAATGGGTAGTTGCAAGTCAGAGAAGTCTCTCTTGAGATAATGGCTGAAT 417
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478 CCAGATATTTATTCATATCATCTCTCCCAAGATGCTGCCATCTAGAAATTCATGTCACTT 537
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838 ACATTATGAAGATGAGCTGAATGGCTTTGTGGA 872

RESULT 6
COI63167 835 bp mRNA linear EST 18-JUN-2004
LOCUS FLDI_39_H09.g1_A029 Root flooded Pinus taeda cDNA clone
DEFINITION FLDI_39_H09_A029 5', mRNA sequence.
ACCESSION COI63167
VERSION COI63167.1 GI:48933708
KEYWORDS EST.
SOURCE Pinus taeda (loblolly pine)
ORGANISM Pinus taeda
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.
REFERENCE 1 (bases 1 to 835)
AUTHORS Pratt,L., Cordonnier-Pratt,M.-M., Lorenz,W.W., Zimmermann,C. and
Dean,J.F.D.
An EST database from flooded loblolly pine (Pinus taeda) roots
Unpublished (2004)
Contact: Cordonnier-Pratt MM

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Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu

RNA prepared and library constructed by W. Walter Lorenz (School of Forest Resources, University of Georgia); plant material prepared by Craig Zimmermann (School of Forest Resources, University of Georgia) using rooted cuttings provided by the Forest Biology Research Cooperative (FBRC) and the CCLONES project at the University of Florida; sequencing done in the Laboratory for Genomics and Bioinformatics, University of Georgia. Sequence ends have been trimmed to exclude vector and regions below Phred quality 16. Three-prime sequences are presented as their reverse complement and have been trimmed to exclude polyA.

Seq primer: JENREV (CAGGAACAGCTATGACC).

FEATURES

source

1. .835
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/notes="Organ: root; Vector: pSL1180; Site_1: EcoRI; Site_2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. Prior to harvesting tissues for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain 5% soil moisture content. Pots holding the rooted cuttings were fully submerged in water for 24 hours prior to harvest of the roots for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."

Query Match 16.2%; Score 428.8; DB 7; Length 835;
Best Local Similarity 71.2%; Pred. No. 9.9e+107;
Matches 587; Conservative 0; Mismatches 222; Indels 15; Gaps 1;

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192 TACTCCCAATGGATTACTGTGAGTCAAGAGAGTCTTTTAGAAGTATGCGAAGATTTCCG 251

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312 TATTACTCTATTCTCTCTCTCAAGTTTGGACCAATAGATATCATGTACGTGTGCT 371

1582 TTAGTATATGGTCAAGCCCTTACCGGAAGGTTTACCGAGGAGTGTGTTTCGACATGGATG 1641

ORIGIN

CO254258 893 bp mRNA linear EST 23-JUN-2004
WS00821.B21_M14 WS-X-N-A-9 Picea glauca cDNA clone WS00821_M14 3',
mRNA sequence.
CO254258
EST. CO254258.1 GI:49137120
Picea glauca (white spruce)
Picea glauca
Picea glauca
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
REFERENCE
AUTHORS
Ralph, S., Kolosova, N., Cooper, D., Butterfield, Y., Kirkpatrick, R.,
Liu, J., Palmquist, D., Scott, J., Barber, S., Yang, G., Babakiff, R.,
Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M.,
Moran, J., Olson, T., Wong, D., Friedmann, M.F., Ritland, C.E.,
Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C.,
Ritland, K. and Bohlmann, J.
The spruce transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
Unpublished (2004)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-6097
Email: bohlmann@interchange.ubc.ca
Plate: WS00821 row: M column: 14
High quality sequence stop: 893.
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1687 AGCTCAAACTTCAAGTTTACAGCTGACCTCCTCAACTCCAAATATATATGTTGGGACCTGGT 1746
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1747 ACAGGTTAGTCTCTTTCAGAGATTTTCGAGGAAAGAAATGCGCCCTCAAGGAAATGGT 1806
552 ACTGGTTTACGACCTTTTACAGGTTTTCGAGGAAAGAGCCGCACTTCAAGAATCTGGA 611
1807 GCTCAACTTGGCCCGACGAGTCTTTTTCGAGATGAGGAATCGTAATATGACATTCATT 1866
612 GCGAAGCTCGGGCCAGCTGTTCTTTTCTTTGGTGAGGAATCGCCAAATGGACTACATT 671
1867 TATGAAGACGAATTAACAACTTCGTGGAAACGAGGAGTCAATTTCCGAGCTAGTTATTGCC 1926
672 TATGAAGATGAATGNAAGAACTATGTGGATCTGGGTATTCACCGATCTTGTCTTGTCT 731
1927 TTTTCACGTGAAGGGGAAAGAAAGAAATATTTTCAACATAGATGATGAGAAAGCAACG 1986
732 TTTCTCTCGTGAAGGAGCAACCAAGAGATATGTGCAGCACAGATAGCAGAGAAGGCATCC 791
1987 GATGTATGGAATGTGATATATCAGGGGACGCTTATCTCTATGTGTG 2030
792 TACATTTGGAATCTCAATTTCTCAAGGTGGCTATCTCTATGTATG 835

RESULT 7

CO254258

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

harvested August 17th
 /lab_host="E. coli DH10B cells"
 /clone_lib="WS-X-N-A-3"
 /notes="Organ: Outer xylem from 25 year old trees harvested at Kalamalka Research Station in Vernon, British Columbia in 2001; Vector: pBluescript II SK (+) XR; Site 1: EcoRI (S' end of cDNA); Site 2: XhoI (3' end of cDNA); mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods (Bonaldo M.F. et al. (1996) Genome Research 6(9):791) in order to reduce the abundance of highly expressed transcripts."

ORIGIN

Query Match	16.1%;	Score 426.4;	DB 7;	Length 893;
Best Local Similarity	70.0%;	Pred. No. 4.7e-106;		
Matches 596;	Conservative 0;	Mismatches 241;	Indels 15;	Gaps 1;
QY	1353	TGAGCAGAGAGATTCGGCTTTTGTTCATCACCCTCTGGGAAGATGATGATTTCAAATG	1412	
DB	3	TGAAGTGGAGAGGTTGAAGTTCTTTCATCACCACCGAAGGATGAGTACTCCCAATG	62	
QY	1413	GGTAGTTGAAGTCACAGAGAGTCTTTGGAGATCATGGCGAGTTCCTCATCAGCAAAACC	1472	
DB	63	GATTACTGTGATCAAGAAGTCTTTTAGAAGAAATGGCAGAGTTTCCATCTGCANAAACC	122	
QY	1473	CCCTCTGGTGTCTTTTGTCTGAGTAGCCCTCGCTTACCGCCCTCGATATTTCTAT	1532	
DB	123	ACCTATTGGTGTCTTTTGTGAGCAATTCGCCCGCTCTGCAACCTCGATATTTCTAT	182	
QY	1533	CTCATCTCTCTAAGTTTGTCTCCCTCAAGAAATCATGTGACGTGCTTTAGTATATGG	1592	
DB	183	TTCTCTCTTCCCAAGGTTTTTCAACCAATAGATACATGTGCATGTGCTCTGGTTATGG	242	
QY	1593	TCAAGCCCTACCGAAGGTTTCAACGAGAGTGTCTGCATGATGATCAAGATCAGTCACT	1652	
DB	243	GCCAGTCCAACTGGCAGATCCATAAAGTGTGTGTTTCAATGGATGAAGATTCAGT	302	
QY	1653	TCCTCAGGA-----TAGCTGGGCTCCTATTTTGTTCGAACGTCAAACTT	1697	
DB	303	GCCTTCTGAGAAAGCCATGATTGTAGCTGGGCACCAGTCTTTGTTCAGACAGTCAAATTT	362	
QY	1698	CAAGTTACAGCTGACCCCTCAACTCAATATCATGTGGGACCTGGTACAGGGTTAGC	1757	
DB	363	CAAAATGCCAGCAGATCCTTCGGTTCCTATTTGTATGTTGGGCCCTCGAACTGGTTTAC	422	
QY	1758	TCCTTTTCAGAGATTTCTGCAGAAAGATGGCCCTCAAGGAAATGGTGTCAACTGG	1817	
DB	423	ACCTTTTACAGGCTTTTTCAGGAAAGGATGACATTCAGAAATCTGGAGAGAGCTTGG	482	
QY	1818	CCAGCAGTGTCTTTTTCGGATGTAGGAATCGTAAATATGAGCTTCATTTATGAAGACA	1877	
DB	483	GCAGCTGTCTTTTTCGGTTCAGGAATCGCAAAATGGACTACATTTATGAAGATGA	542	
QY	1878	ACTAAACACTCTGGAGAGGAGTCAATTCGGAGCTAGTTATTTGCCCTTTTCAGTGA	1937	
DB	543	ACTGAAGAACTATGTGGAAATGGTGTATTTAGTGTATCTGGTCTTCTCTCGCA	602	
QY	1938	AGGGGAAAGAGGAATATGTTCAACATAAGATGATGGGAAAGCAACGGATGTATGGAA	1997	
DB	603	AGGAACAAACAAAGATATGTGCAGACCAAGATTACAGAAAGGCACTCATTTATTTGGAA	662	
QY	1998	TGTGATATCAGGGGACGGTTATCTCTATGTGTGTGTGTATGCCAAGGGAAATGCCACAGA	2057	
DB	663	TCTTATTTCTCAAGGTGGCTATCTCTATGTATGTGTGTGTATGCCAAGGGCAATGCTAGGGA	722	

QY	2058	TGTCATGCGCAGTTGCTATACCATTTGCCCAAGAACAGGAGCCCATGGAATCATCTCTGTC	2117	
DB	723	TGTGCACAGGCGCTACACAATATTTGTCCAGAGCAGGAATCAGTGGATAGCAGCATGTC	782	
QY	2118	CGAAGCTGCAGTAAAGAACTCCAAGTTGTAAGAACGATATCTTAAGAGATGTCTTGGTGATC	2177	
DB	783	AGAGGCTACAGTGAAGAAATTTACAGACAGAGAGAGATATTTACGAGATGTATGGTAGTT	842	
QY	2178	GAATGTAGCTTG 2189		
DB	843	GAGTGAATTTTG 854		
RESULT 8				
LOCUS	CO166163	806 bp mRNA linear EST 18-JUN-2004		
DEFINITION	FLD1_59_F08_A029 Root flooded Pinus taeda cDNA clone			
ACCESSION	CO166163	FLD1_59_F08_A029 5', mRNA sequence.		
VERSION	CO166163.1	GI:48936704		
KEYWORDS	EST.			
SOURCE	Pinus taeda (loblolly pine)			
ORGANISM	Pinus taeda			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.			
AUTHORS	Pratt, L., Cordonnier-Pratt, M.-M., Lorenz, W.W., Zimmermann, C., Johnson, H., Anfuso, C., Kamran, D., Chhabra, D., and Dean, J.F.D.			
TITLE	A loblolly pine (Pinus taeda) EST database from flooded roots			
JOURNAL	Unpublished (2004)			
COMMENT	Other ESTs: FLD1_59_F08_b1_A029 Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA Tel: 706 542 1860 Fax: 706 583 0210 Email: mmpratt@uga.edu			
FEATURES				
source				
	1..806	Location/Qualifiers		
	/organism="Pinus taeda"			
	/mol_type="mRNA"			
	/strain="3 CCLONES"			
	/db_xref="taxon:3352"			
	/clone="FLD1_59_F08_A029"			
	/lab_host="DH10B-TI phage-resistant E. coli"			
	/clone_lib="Root flooded"			
	/note="Organ: root; Vector: pSL1180; Site 1: EcoRI; Site 2: XhoI; The library was prepared from polyA+ RNA from the roots of 1-year-old loblolly pine (Pinus taeda) cuttings that were rooted and then planted in washed sand. Prior to harvesting tissues for RNA isolation, the rooted cuttings were maintained for 27 days (April 2003) under ambient conditions in a local greenhouse. They were kept on a weekly regimen of 0.5x nutrient-complete Hoagland's solution and supplemented with additional water sufficient to maintain 5% soil moisture content. Pots holding the rooted cuttings were fully submerged in water for 24 hours prior to harvest of the roots for RNA isolation. Double-stranded cDNA was cloned unidirectionally into pSL1180. Inserts can be excised with EcoRI (5' end) and XhoI (3' end)."			

```
ORIGIN
Query Match      15.9%; Score 421; DB 7; Length 806;
Best Local Similarity 71.4%; Pred. No. 1.4e-104;
Matches 575; Conservative 0; Mismatches 215; Indels 15; Gaps 1;

QY 1273 CTAGCAGCGTATGCTGATCTTTTGAATCCCTCTAGAAAGCGTCTCTGATTGCTCTGTCC 1332
DB 2 CTTGCTGTTTGCAGATTGTTGAACTCCCTCTTAATGCTGCTGCTGCTGCTGCTGCT 61

QY 1333 GCTCATGCTATCTGATCCAGTGAAGCAGAGAGATGCGGCTTTTGTGATCATCACTCTGGGA 1392
DB 62 AGTCATGCTATCTGATCCAGTGAAGCTGAGAGGTGAAGTTTCTTTCATCACCAGCGCGA 121

QY 1393 AAGAATGAGTATTCARAAATGGTAGTTGGAAGTCAGAGGAGTCTTTGGAGATCATGGCC 1452
DB 122 AAGATGAGTACTCCCAATGGATTAATGAGTCAAGAGGAGTCTTTTGAAGTAATGGCA 181

QY 1453 GAGTTTCCATCAGCAAAACCCCTCTTGGTGTGTTCTTTGCTGCAGTAGCCCTCGCTTA 1512
DB 182 GAATTTCCGCTCGAAACCACTCTCGGTGTCTTCTTGCGCAATTTGCCACGCTG 241

QY 1513 CCCTCTGATATCTATCTATCTCTCTCTTAAGTTGCTCTCTCAAGAATTCATG 1572
DB 242 CAACCTCGATATCTATCTCTCTCTCTCAAGTTTGCACCCCAATAGATACATGTA 301

QY 1573 ACCTGTGCTTTAGTATGCTCAAGCCCTACCGGAGGGTTTCCACGAGGAGTGTCTG 1632
DB 302 ACCTGTGCTCTGTTTATGGCTTAGTCTCAAGTGGCAGATTCACAAAGGTGTTGTTC 361

QY 1633 ACATGGATGAAGCATGCTGCTCTCAGGA-----TAGCTGGGCTCTCTATT 1677
DB 362 AATTGGATGAAGAAATTCGGTCTCTCTGAGGAATCTTGTAGTGGGACCACTC 421

QY 1678 TTTGTTGGAAGCTCAAACTTCAAGTACAGAGTACAGCTGACCCCTCAACTCAATATCATGGTG 1737
DB 422 TTTGTTGAGACAGTCAAAATTTCAAAATGCGCAGAGATCTTCACTTCTTATGTTGTTG 481

QY 1738 GGAACCTGTTGACGGTTAGTCTCTTTTCAGAGGATTTCTGAGAAAGATGCGCCCTCAAG 1797
DB 482 GGCCTTGGAACTGGTTTAGCCTTTTAGAGGTTTTTTCAGAAAGAGCCGCACTTCAA 541

QY 1798 GAAATGGTGTCTCAACTTGGCCAGCAGTGTCTCTTTTCGAGTATGAGGAATCGTAATATG 1857
DB 542 GAATCTGGAGGAGTCTGGCCAGCTGTCTTTCTTTGCTGAGGAATCGCCAAATG 601

QY 1858 GACTTCAATTTATGAAGCAAGCACTAAACAACTTCGTGGAACGAGGAGTCAATTCGGAGCTA 1917
DB 602 GACTACATTTATGAAGATGAATGAAGAACTATGTGATATCTGGCGTATTTGACCGATCT 661

QY 1918 GTTATTCCTTTTCAGTGAAGGGAAGAGGAATATGTTCAACATAGATGAGGAG 1977
DB 662 GTTCTTCTCTCTCGTGAAGGAGCAACCAAGAGTATGTGAGCAGCAAGATAGCAGAG 721

QY 1978 AAAGCAACGGATATGAGGATGTGATATCAGGGGAGCGTTATCTCTATGTGTGTGTGAT 2037
DB 722 AAGGCATCTACATTTGGAATCTCAATTTCTCAAGGTGGCTAATCTATGTGTGTGAT 781

QY 2038 GCCAAGGGAATGCCAGAGATGTC 2062
DB 782 GCCAAGGGATGGCTAGGGATGTC 806

RESULT 9
CO084955
LOCUS
DEFINITION GR_Ea01N07.f GR_Ea Gossypium raimondii cDNA clone GR_Ea01N07 5', mRNA sequence.
ACCESSION CO084955
VERSION CO084955.1 GI:48775589
KEYWORDS EST.
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosids; eurosids II; Malvales; Malvaceae;
Kim.H., Yu.Y., Kudrna,D., Hatfield,J., Stum,D., Mueller,C.,
Udall,J.A., Rapp,R.A., Wendel,J.F., Rao,K., Soderlund,C. and
Wing,R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 01 row: N column: 07.
Location/Qualifiers
1..907
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Ea01N07"
/tissue_type="whole seedlings"
/dev_stage="first true leaves"
/lab_host="DH10B"
/clone_lib="GR_Ea"
/note="Vector: pCMV.SPORT-6.1; Site_1: NotI; Site_2:
EcoRV; library made by invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AGI. More glycerol clones held in -80."
```

```
QY 1621 GGAGTGTTCGACATGATGACGATCGAGTTCC-----TCAGGATAGC 1665
Db 541 GGTGTTGTTCAACTTGGATGAAGAATGCTGTCTCTCGGGAAAAAGCGATGATCGAGC 600
QY 1666 TGGGCTCCTATTATTTTGTTCGAACGTCAAACTTCAAGTTACCACTGACCCCTCAACTCCA 1725
Db 601 TGGGACCCCAATTTTGTTCAGGCAATCAAACTTTAACTTCCTTCAGATGCTAAAGTGCC 660
QY 1726 ATTATCATGTTGGACCTGATGACAGGTTAGCTCCTTTTCAGAGGATTTCTTCAGAGAAAGA 1785
Db 661 ATCATTAATGATTGGCCCTGCTACTGATGCTCCTTTTCAGGGGATTCCTTCAGGAAAGG 720
QY 1786 ATGGCCCTCAGAGAAATGTTGCTCAACTTGGCCCGACGAGTGTCTTTTCGATGTAGG 1845
Db 721 CTTGCACTGAAGAAGCTGGTGTCTGAGTTGGGTCCATCTGTATTGTTTCTTGGCTGCAGA 780
QY 1846 AATCGTAATATGCACTTCATTTATGAAGACGAACTAAACAACTTCGTGGAACGAGGAGTC 1905
Db 781 AACCAGGAATGATTTTATATATGAGATGAGCTCAACAACTTTGTCAACAGTGTGTGA 840
QY 1906 ATTTCGAGCTAGTTATGCTTTTTCACGTGAAGGGGAAAGAAAGAAATATGTCA 1961
Db 841 CTATCTGAGCTTGTGTTGCTTTTTCACGTGAGGGACCTACCAGGGAATATGTGCA 896
```

RESULT 10

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CK271587
LOCUS CK271587
DEFINITION EST17665 potato abiotic stress cDNA library Solanum tuberosum cDNA
clone POAD011 5' end, mRNA sequence.
VERSION CK271587
KEYWORDS
SOURCE Solanum tuberosum (potato)
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum.
1 (bases 1 to 928)
Buell,C.R., Hart,A., Zismann,V., Karamycheva,S.A. and Baker,B.
Generation of ESTs from abiotic stressed potato tissue
Unpublished (2003)
Other ESTs: EST17666
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from the University of Arizona Genomics
Institute via http://genome.arizona.edu/orders/
Seq primer: ATT TAG GTG ACA CTA TAG.
```

FEATURES

```
source
1..928
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="FOAD011"
/tissue_type="abiotic stress treated leaf and root tissue"
/lab_host="DH10B-TonA"
/clone_lib="potato abiotic stress cDNA library"
/notes="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: Solanum tuberosum var. Kennebec plants were
grown from cuttings on a 16hr light/8 hr dark cycle at 25
C for 3-4 weeks. Abiotic stress conditions were applied to
four separate sets of plants. Set 1 involved saturation of
the soil with 150 mM NaCl and tissues were harvested at
following application of the salt stress (leaves: 2hr,
6hr, 12hr, 1d, 2d, and 4d; roots: 2hr, 6hr, 12hr, and 2d).
Set 2 were grown under the standard conditions and then
were water stressed by withdrawal of further watering
applications. Drought stressed plants were harvested after
cessation of watering (leaves: 3d, 5d, and 7d; roots: 3d
and 5d). Set 3 were grown under the standard conditions
```

and then were cold stressed by placement at 4 C. Cold stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, and 4d and roots were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d. Set 4 were grown under the standard conditions and then were heat stressed by placement at 35 C. Heat stressed leaves were harvested at 2 hr, 6 hr, 12 hr, 1 d, 2d and 4d and heat-stressed roots were harvested at 6 hr, 12 hr, 1 d, and 4d. RNA was isolated from all tissues and equal RNA from each tissue and stress was pooled to construct the cDNA library. RNA sample."

ORIGIN

```
Query Match 15.8%; Score 418.8; DB 7; Length 928;
Best Local Similarity 68.6%; Pred. No. 6e-104;
Matches 608; Conservative 0; Mismatches 272; Indels 6; Gaps 2;

QY 337 GAAGTTGATCTCGGTAAATAAAGCTCACTATATATTTTGGTACTCAGACTGTACTGCT 396
Db 36 GAGATTGATGATGGAAGAAGAGGTTACCATATTTTTCGGAACCCAGACTGTGTACGA 95
QY 397 GAAGGATTTGCTAAGGCATTGGCAGAGAAATTTAAGGCAAGGTACAAAGAAAGCAGTTGT 456
Db 96 GAAGGCTTCGCAAGGCACTTCTGAGGAAGCAAGGCCAGATATGAGAAGGCTGTCTTT 155
QY 457 AAAGTAGTTGACCTGGATGACTATGCGCCGAGGATGATCAATATGACAGAAATTTAAAG 516
Db 156 AAAGTCATTGATGATGATGATTTATGCGGCTGATGATGAAGAGTATGAAGAAAATTTGA 215
QY 517 AAAGAGTCTTTGCTGTTTTTCATGTTAGGCACCTTATGTTGATGTTGAGCCAACTGCAAT 576
Db 216 AAAGAAATTTGGCATTCTTTTCTTGGCGCATATGAGAGATGTTGAAACCACTGATAT 275
QY 577 GCTGCGAGATTTTACAAATGTTTCACTCAGAAACATGAAAGGGGAGAGTGGCTTCAGCA 636
Db 276 GCTGCCAGATCTATAAATGTTTGAAGAGGGGAAAGAGAGGGGTGACTACTTTTAAAAAT 335
QY 637 CTAACTTATGTTGTTTTTGGTTTGGGTAAACCGTCAATACAGCANTTTCAACAGATCGCG 696
Db 336 CTTTCAATATGAGATATTTGGGCTTGGTAAACAGGCAATACAGCANTTTTAAACAGATTGCT 395
QY 697 GTAGATGTGGATGAGCAACTCGGTAAACAAAGGTGCAAGCGCATTTGTTCAAGTGGGGCTC 756
Db 396 AAAGTTGTGGATGAGCTTCTGCTGAGCAAGCGGGCAGAGGCTTGTTCAGTGGGTCTT 455
QY 757 GTGACGATGATCAATGCAATGCAAGATTTTATCTGTTGGCGAGAAATGTTGTGCACT 816
Db 456 GGAGATGATGATCAATGCAATGCAAGATTTTGTGTCATGCGCTGAGTTACTGTGCGCCT 515
QY 817 GAATTGGATCAGTTGCTCAAGATGAGGATGCTGCTCCTTTCAGTGGCTACACCGTATATT 876
Db 516 GAATTGGATAAGTTGCTTCTTGTGGGATGATGCAACT--GCTGCAACTCCATATACT 572
QY 877 GCTACTGTTTCTGAATACAGGCTAGTGTATTACGAAACTTACCGTTCGCGCTCTGGAATGAT 936
Db 573 GCTGCAGTTTGGATATAGGTTATTACCTATGAGAAGTCCCACTTTGATAACGACTTG 632
QY 937 AAACACATAAA---TACTGTAAACGCGAGTTTGCATTTGATATTCTCATCTCTTCGACGA 993
Db 633 ACCAACACAAATGGTCATCAAAATGGACATGTCATTGTTGATGAACTGGTGCATCATCTGTG 692
QY 994 ACCATTGTTGCTCAACAAAGAGAGCTCCACAAACCCAGTCTGATAGATCTCTGTATACAT 1053
Db 693 GCTAATGTTGCTGTGAGGAAGGAGCTTCATCCGAGCTTCTGATGCTTCTTGTGCACTCAT 752
QY 1054 CTGGAGTTTCGACATATCAGGCTCTTTCCCTTTACATATGAGACTGGAGATCATGTTGGTGT 1113
Db 753 CTGGAGTTTGACATTTCTGGCACTGACCTTGTGTATGAACTGGTGCATCATGTTGGTGTG 812
QY 1114 TATGCTGAGAACTGGATGAAAATCTGCGAGGAAGCAGGGAAGCTGTTGGGTCAACCCCTG 1173
Db 813 TACTGTGAAAATTTTATTGAAAACCGTGGAGGAGCTGAAAGGTTACTGAATATATCACCG 872
QY 1174 GATTTGCTGTTTTCAATTCAACGGGATAAAGAGCGGGGTCAACCC 1219
```


TITLE Generation of ESTs from tomato fruit tissue, breaker stage (2002)
JOURNAL Unpublished (2002)
COMMENT Contact: CUGI
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: <http://www.genome.clemson.edu/orders/index.html>
This clone is available through the Clemson University Genomics Institute
Seq primer: T3.

FEATURES

source
1..729 Location/Qualifiers
/organism="Lycopersicon esculentum"
/mol_type="mRNA"
/cultivar="TA496"
/db_xref="taxon:4081"
/clone="GLEG64N20"
/tissue_type="Pericarp"
/dev_stage="breaker"
/lab_host="SOLR"
/clone_lib="tomato breaker fruit"
/note="Vector: pBluescriptSKmCUadapt; Site 1: EcoRI; Site 2: XhoI; supplier: Boyce Thompson Institute; sequencing: The Institute for Genomic Research. Fruit were harvested at the breaker stage (first sign of lycopene accumulation on the blossom end of fruit). Fruit were cut in half and the seeds and locules were discarded prior to freezing the pericarp."

ORIGIN

Query Match 15.6%; Score 413.8; DB 4; Length 729;
Best Local Similarity 74.3%; Pred. No. 1.3e-102; Indels 15; Gaps 1;
Matches 542; Conservative 0; Mismatches 172

1424 GTGAGGAGTCTTTTGGAGATCATCGCGAGTTTCCATCAGCAAAACCCCTCTGGTG 1483
Db 1 GTCARAGAATCTTATGAAGTAATGCTGAGTTTCCATCGGCAAGCCTCCCTTGGTG 60

1484 TGTCTTTTGTGAGTAGCCCTCGCTTACCGCTCGATACATTTCTATCTCATCTCTC 1543
Qy 61 TATTTTTTGCAGCAGTTGCGCCTCGTTTACAGCCTCGCTACTATTCAATCTCATCTC 120

1544 CTAAGTTTCTCCCTCAAGAATTCATGTCAGCTGTCTTTAGTATATGTCGAAGCCCTA 1603
Qy 121 CTCGATTTGCACCGCTAGAGTCCATGTAACCTGTGCATGTCTATGTGTCACACTCCCA 180

1604 CCGGAAGGGTTACCGAGGAGTGTGTTGCACATGGAATGAAGCATGTCAGTTCTCTCAGGA-- 1661
Db 181 CTGGCCGAATTCATAAAGGAGTGTGTTCAACTTGGATGAAGAGTGCAGTACCTTCGGAGA 240

1662 -----TAGCTGGCTCCTATTTTGTTCGAACGTCGAACCTTCAAGTTTACCAG 1708
Qy 241 AAAGTCACAATTTGCAGCTCTGTCTCCATTTTCAATTAGGCCATCTAATTTCAAATTACCAG 300

1709 CTGACCCCTCAACTCCAATTTATCATGTGGACCTGTGACAGGTTAGCTCTTTTCAGAG 1768
Qy 301 CCGACCTTCAATTCGAATTTGATGTTGGGGCTGGAGTGTGTTGGCACCATTACGGG 360

1769 GAATTTCTGAGGAAGAAATGGCCCTCAAGGAAATGGTGCTCAACTTGGCCCGCAGAGTGC 1828
Qy 361 GATTCCTGAGGAAGAGCAGCATTCGAAGAGATGCGCTCAACTTGGTCTGCTTTAC 420

1829 TCTTTTTCGATAGGAATCGTAATATGGAATTCATTTATGAAGACGAATTAACAAT 1888
Qy 421 TGTGTTTTCGTTGTAGGAATCGTAGAATGGAATTTATTTATGAGGAAGAGCTTCAGAGTT 480

1889 TCGTGAACAGGAGTCATTTTCGAGCTAGTTATTTCCCTTTTCACTGTAAGGGGAAAGA 1948
Qy 481 TTGTGGAATCAAGTGTAATATCAGACTGATTTATTCATTTTCAAGGGAAGGTTACAGA 540

1949 AGGAATATGTTCAACATAAGATGATGAGGAAGCAACCGGATGTATGGAAATGTGATACAG 2008
Qy 541 AAGAGTATGTTCAACACAAATATGATGAAAGGCTTCCCATGTTTGGAGTTTAAATCTCTC 600

Qy 2009 GGGACGGTTATCTCTATGTGTGTGTGATGCCAAGGGAATGGCCAGAGATGTCCTCATCGCA 2068
Db 601 AGGAGGGATATCTATATATGTATGTGGGATGCTAAAGGGATGGCCAGAGACGTACATCGTA 660

2069 CTTTGCATACCAATTCGCCAAGAACAGGGACCCATGGAATCATCTGTCGGAAGCTGCAG 2128
Qy 661 CACTCATACCAATAGTCCAGGAGCAGGAGATGCGGACTCATCCAAAGCAGAGGCTGTTG 720

2129 TAAAGAAAC 2137
Qy 721 TAAAGAAAC 729
Db

RESULT 13
BUB13507
LOCUS
DEFINITION BUB13507 Populus bark cDNA library Populus tremula x Populus tremuloides cDNA 5 prime, mRNA sequence.
ACCESSION BUB13507
VERSION BUB13507.1 GI:23969749
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Malpighiales; Salicaceae; Populus.
1 (bases 1 to 690)
REFERENCE Unneberg,P., Bhalerao,R.R., Jansson,S. and Sterky,F.
AUTHORS The poplar tree transcriptome: Analysis of expressed sequence tags from multiple libraries
TITLE Unpublished (2002)
JOURNAL Contact: BHALERAO RUPALI R.
COMMENT Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.

FEATURES
source
1..690
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/tissue_type="bark"
/clone_lib="populus bark cDNA library"

ORIGIN
Query Match 15.6%; Score 413.6; DB 5; Length 690;
Best Local Similarity 76.8%; Pred. No. 1.5e-102; Indels 15; Gaps 1;
Matches 525; Conservative 0; Mismatches 144

1218 CCAGGGAAGCTCATTTACCACCTCTCTTCCAGAGTCTCTTCCAGCTTACGATCTGCCCTAGC 1277
Db 7 CCGGGGAAGCTCATTTGCCACCTCTTCCAGTCCCTGCGACACTTCACACTGCATTGCG 66

1278 AGCTATGCTGATCTTTTGAATCTCTCTAGAAAGGCTTCTCTGATGCTCTGTCCGCTCA 1337
Qy 67 ATGCTATGCAGATCTCTTGAGCCCTCCTAAAAGGCTGCTTTGCTTGTCTGCTCTCA 126

1338 TGCATCTGTACCAGTGAAGCAGAGAGATTGCGCTTTTGTCTCATCACCTCTCGGAAAGAA 1397
Qy 127 TCCAGTGAACCTAGCGAGCAGATAGACTCAAGTTTTTATCATCCCGAAGAAAGAA 186

1398 TGAGTATTTCAAAATGGGTAGTTGGAAGTCAGAGGAGTCTTTTGGAGATCATGCGCAGTT 1457
Qy 187 TGAATACTCTCACTGGGTCAATGCGCAAGTCAGAGAAGTCTTCTCGAGGTAAATGGCTGAGTT 246

1458 TCCATCAGCAAAACCCCTCTTGGTGTGTTCTTTCTGTCAGTAGCCCTCGCTTACCGCC 1517
Qy 247 CCCATCTTTCAAAACCTCCCTTGGTATCTTTTGTGTCAGTGGCACCCCGCTACAGCC 306

1518 TCGATACTATTCTATCTCATCTCTCCTAAGTTTGTCTCCTCAAGAAATTCATGTGACGTG 1577


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Db      843 NTCTANGTAT 853
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Gossypium raimondii
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
1 (bases 1 to 824)
Kim H., Yu Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J.A., Rapp, R.A., Wendel, J.F., Rao, K., Soderlund, C. and
Wing, R.A.
Global assembly of Cotton ESTs
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
Plate: 0041 row: E column: 04.
Location/Qualifiers
1. 824
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/dev_stage="3 to +3 DPA"
/lab_host="DH10B"
/clone_lib="GR_Eb"
/notes="Vector: pCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV; Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by AgI. More glycerol clones held in -80."

FEATURES
    source
    1. 824

Query Match      15.5%; Score 411; DB 7; Length 824;
Best Local Similarity 70.6%; Pred. No. 8.3e-102;
Matches 584; Conservative 0; Mismatches 225; Indels 18; Gaps 2;

QY 1226 GCTCATTACACCTCTTTCCAGGTCCTTGACCTTACGATCGCCCTAGCACGCTATG 1285
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QY 1286 CTGATCTTTTGAATCTCTCTAGAAAGGCTTCTGATGCTCTGTCGGCTCATGATCTG 1345
Db 58 CTGATCTTTTGAAGCTCACCACCAAAAGTCTGCTTTACTTGTCTGCTGGCTGCTCATGCTCTG 117

QY 1346 TACCCAGTGAAGCAGAGAGATTCGGCTTTTGTGCATCACCTCTGGGAAAGAGATGATTT 1405
Db 118 ATCCCACTGAGCTGATGCTAGCTAAGACACCTTCATCGCCAGCTGGAAAGGATGAATATG 177

QY 1406 CAAAATGGGTAGTTGGAAGTCAGAGAGTCTTTTGGAGATCATGCGCGAGTTTCCATCAG 1465
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QY 1466 CAAAACCCCTCTTGGTGTGCTTTTGTGTCAGTAGCCCTCGCTTACCGCTCGATCT 1525
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QY 1526 ATTCTATCTCATCTCTCTAAAGTTGTGCTCCCTCAAGAAATTCATGTGAGTGTGCTTTAG 1585
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Db 778 TCTGGAACATGATTTCTGAAAGAGGTTACCTATATGTGTGTGGTGTAT 824

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Job time : 7667 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 18, 2005, 09:24:07 ; Search time 455 Seconds
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Gapop 10.0 , Gapext 1.0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	165.6	6.3	2403	4	US-09-023-655-1226
4	118.4	4.5	260	4	US-09-313-294A-2366
5	111.8	4.2	3037	4	US-09-911-781-10
6	111.8	4.2	3037	4	US-10-400-902-10
7	111.8	4.2	4145	3	US-09-302-620B-82
8	111.8	4.2	4145	4	US-09-912-161-5
9	111.8	4.2	4145	4	US-09-911-781-3
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12	108	4.1	4206	4	US-09-912-161-3
13	108	4.1	4206	4	US-09-911-781-2
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25	86.2	3.3	3150	4	US-10-018-730A-3
26	84.8	3.2	170	4	US-09-313-294A-3539
27	84	3.2	1713	4	US-09-248-796A-4447

ALIGNMENTS

RESULT 1

US-09-627-216A-13
; Sequence 13, Application US/09627216A
; Patent No. 6368837
; GENERAL INFORMATION:
; APPLICANT: Sariafani, Sima F
; APPLICANT: Tang, Xiao-Song
; APPLICANT: Qi, Wei Wei
; APPLICANT: Vannelli, Todd
; APPLICANT: Gatenby, Anthony
; TITLE OF INVENTION: Bioproduction of para-Hydroxycinnamic Acid
; FILE REFERENCE: BC1009 US NA
; CURRENT APPLICATION NUMBER: US/09/627,216A
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Helianthus tuberosus
US-09-627-216A-13

Query Match	30.5%	Score	807.6;	DB	3;	Length	1863;
Best Local Similarity	67.2%	Pred. No.	6.9e-236;				
Mismatches	1197;	Conservative	0;	Mismatches	559;	Indels	24;
Gaps	3;						
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; Sequence 13, Application US/09765873A
; Patent No. 6521748
; GENERAL INFORMATION:
; APPLICANT: Tang, Xiao-Song
; TITLE OF INVENTION: BIOPRODUCTION OF PARA-HYDROXYCINNAMIC ACID
; FILE REFERENCE: BC1009 US CIP
; CURRENT APPLICATION NUMBER: US/09/765,873A
; CURRENT FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 09/627,216
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 60/147,719
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 13
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Helianthus tuberosus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1764)
US-09-765-873A-13

Query Match 30.5%; Score 807.6; DB 4; Length 1863;
Best Local Similarity 67.2%; Pred. No. 6.9e-236;
Matches 1197; Conservative 0; Mismatches 559; Indels 24; Gaps 3;

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Qy 1435 CTTTGGAGATCATGGCCGAGTTTCCATCAGCAAAACCCCTCTGTTGTTCTTGTCT 1494
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Db 1072 GCTATTGCCCCGGTTTTCAGCTCGATCTACTATCTTCTCTCCCAAGATGGA 1131
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Db 1132 CCCAACAGGATTCATGTTAGCTGTGATTAATGTTATGAGAAGACTCTCTGGAGGTCTATC 1191
Qy 1615 CACGAGGATGTTTCGACATGATGAGCTGAGCTTCT-----CAG 1659
Db 1192 CAAAAAGGAATATGCTCAACCTGGATGAAGAAATGCTGTGCTTTGACCGGAATAAAGAT 1251
Qy 1660 GATAGTGGGCTCTATTTTGTTCGAACCTCAAACTTCAAGTTACGAGTGAACCCCTCA 1719
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Qy 1720 ACTCCAAATATCATGTGGGACTGTTGATGAGGTTAGCTCTTTCAGAGATTTCTGAG 1779
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Db 1372 GAAAGATTAGCTCTCAAGGAATCTGAAACCGAACTCGTCAATCCATTTTGTCTTCGGT 1431
Qy 1840 TGTAGGAATCGTAATATGGACTTCATTTATGAAGAGAACTAAACAACTTCGTGGAAACGA 1899
Db 1432 TGCAGAAACCGTAAAGTGGATTTCAATATGAGAAATGAACCTGAACAACTTTGTTGAAAT 1491
Qy 1900 GGAGTCAATTCGAGCTAGTTATTGCTTTTACGTTGAAGGGGAAAGAGGAATATGTT 1959
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Qy 2080 ATTGCCCAAGAACAGGACCCATCGAATCATCTGCTGCCGAGCTGAGTAAAGAACTC 2139
Db 1672 ATTGTCAAGAACAGGGAATTTGGATTCCTCTTAAAGCAGAGCTGTATGTGAAGAACTCA 1731
Qy 2140 CAAAGTTGAAGAACGATATCTAAGAGATGTCTGATGATCGA 2179
Db 1732 CAAATGTCGGAGATACCTCCGTGATTTGTTGATCTA 1771

RESULT 3

US-09-023-655-1226
; Sequence 1226, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREWITH
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1226:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2403 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear		
; IMMEDIATE SOURCE:		
; LIBRARY: GENBANK		
; CLONE: 9247306		
US-09-023-655-1226		
Query Match		
Best Local Similarity 47.0%; Pred. No. 2,2e-39;		
Matches 793; Conservative 0; Mismatches 839; Indels 54; Gaps 7;		
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Db	392	TGTTGTTTTCATGGTAGCCACATATGGTATGCTGAGCCAACTGACAAATGCTGCGAGAT 451
QY	587	TTTACAAATGGTTCACTCAGGAACATGAAGAGGGGAGAGTGGCTTCAGCAACTAACTTATG 646
Db	452	TCTACGACTGGCTG-----CAGGAGACAGAGCTGGATCTCTCTGGGGTCAAGTTG 502
QY	647	GTGTTTGGTTGGTTAAGCGTCAATACGAGCATTTCAACAGATTCGCGGTAGATGTGG 706
Db	503	CGGTGTTTGGTTGGTTAAGCGTCAATACGAGCATTTCAATGCGCATGGGCAAGTACGTGG 562
QY	707	ATGAGCAACTCGGTAAACAGGTGCAAGAGCGCATTTGTTCAAGTGGGGCTCGGTGAGATG 766
Db	563	ACAGCGGCTGGAGAGCTCGGCGCCAGCGCATCTTTGAGCTGGGGTTGGGCGAGCAG 622
QY	767	ATCAATGCAATTGAAGATGATTTTACTGCTTTGGCGAGAAATTTGTTGGACTGMAATTGGATC 826
Db	623	ATGGGAATTTGGAGGAGGACTTCATCACCTGGCGAGAGCAGTTCTGGCGCGCGTGTGTG 682
QY	827	AGTTGCTCAAGATGAGGATGCTGCTCTTCAGTGGGTAACCGTATATGTTACTGTTTC 886
Db	683	A--ACACTTTGGGGTGGAAAGCACTGGCGAGGAGTCCAGCATTCGCGAGTACGAGCTTG 739
QY	887	CTGAATACAGGTTAGTATTACAGAACTACGCTCGCGGCTCTGGATGATAACACATAA 946
Db	740	TGTTCCACACCGACATAGATGCGGCGCAAGGTGTACATGGGGAGATGGCGCGGCTGAAGA 799
QY	947	ATACTGCTAACCGCGATGTTTGCATTTTGAATTTCTCCATCCTTGCAGAACCATTTGTTGCTC 1006
Db	800	GCTACGAGAACCAAGAGCCGCCCTTTGATGCCAAGAATCGTTCTCGGTGCACTCACCA 859
QY	1007	AACAAGAGAGCTCCACAAACCCAGTCTGATAGATCTGTATACATCTGGAGTTGCGACA 1066
Db	860	CCAAACCGGAAGCTGAACCAAGGAA---CCGAGCGCCACCTCATGCACTTGGAAATTGGACA 916
QY	1067	TATCAGGCTCTCCCTTACATATGAGACTGGAGATCATGTTGGTGTATTATGCTGAGAAT 1126
Db	917	TCTCGGACTCAAATCAGGTATGAATCTGGGACCAACGTTGGTGTGTATCCGAGCCACG 976
QY	1127	GCATGAAACTGTCGAGGAAGCGGGAAGCTGTTGGGTCAACCCCTGGATTTTGTCTGTTT 1186
Db	977	ACTCTGCTCGTCAACAGCTGGGCAAAATCTCTGGTGGCGACCTGGAGCTGTCATGT 1036
QY	1187	CAATTACACGGATAAAGAGAGCGGTACCCAGGAGACTCATTTACACCTCTCTTTC 1246
Db	1037	CCCTGAACACCTGGATGAGGAGTCCAAACGAAG-----CACCCATTC 1081
QY	1247	CAGTCTCTTGCACCTTACGATCTGCCCTAGCAGCTATGCTGATCTTTTGAATCTCTTA 1306
Db	1082	CGTGCCTAGCTCTTACCGCACCGGCTCTACCTACTCTGGAGCATCAACACCCGCGC 1141
QY	1307	GAAAGGCTCTCTGATGTTCTGTCCGCTCATGCTGTGACCCAGTGAAGCAGAGAT 1366
Db	1142	GTACCAAGCTGTGTAGAGCTGGCGCAGTACGCTCGGAGCCCTCGGAGCAGGAGCTGC 1201
QY	1367	TGCGCTTTTG-----TCATACCTCTGGAAAGATGATGATTCAAATGGGTAGTTG 1420
Db	1202	TGCGCAAGATGGGCTCTCTCTCGGCGAGGGCAAGGAGCTGTATCCTGAGCTGGGTGG 1261
QY	1421	GAAGTACAGAGAGTCTTTTGGAGATCATGGCCGAGTTTCCATCAGCAAAACCCCTCTTG 1480
Db	1262	AGCCCCGAGGCACATCTTGCCCATCTGCGAGACTGCGCTCCCTCGGCGCCCTCCCAT-- 1319

1481 GTGTGTTTTCATGGTAGCCACATATGGTATGCTGAGCCAACTGACAAATGCTGCGAGAT 1540

1320 -CGACCACCTGTGTAGCTGCTGCGCGCTGACGAGCCGCTACTACTCATCCCTCAT 1378

1541 CTCCTAAGTTTGTCTCCCTCAAGAAATCATGTGACGTGTCTTTAGTATATGTTGTTCAAAGCC 1600

1379 CTTCAAGGTTCACCCCAACTCTGTGTCACATCTGTGCGGTGGTTGTGGAGTACGAGACCA 1438

1601 CTACCGGAAGGTTCAACCGAGGAGTGTGTTTCACACATGGAATGAAGCATGCAGTTCTTCAGG 1660

1439 AGCCCGGCGCATCAACAGAGGCTGGCCACCAACTGGCTGCGGGCAAGAGCCTGTGCG 1498

1661 -----ATAGCTGGGCTCTCTATTTTGTTCGAACGTCAAACTCTCAAGTTAC 1705

1499 GGGAGAACGGCGCGCTGGTGGTCCCATGTTGCTGCGCAAGTCCCAGTTACGCTGC 1558

1706 CAGTGACCCCTCAACTCCAATTATCATGTTGGGACCTGGTACAGGTTAGCTCTTTC 1765

1559 CTTCAAGGCCACCAAGCTGTCTATGTTGGGCGCCGCGCACCGGGTGGCACCTTTTCA 1618

1766 GAGGATTTCTGAGGAAAGAAATGGCCCTCAAGGAAATGGTCTCAACTTTGGCCCGAGCAG 1825

1619 TAGGCTTCACTCAGGAGCGGGCTGGCTGCGACGACGAGGCAAGAGTGGGGGAGACGC 1678

1826 TGCTCTTTTTCGGATGTAGGAATCGTAATATGGAATTTTATGAAGACGAACTAAACA 1885

1679 TGCTGTACTACGGCTGCGCGCTCGGATGAGGACTACCTGTACCGGGAGGAGCTGGCGC 1738

1886 ACTTGTGGAACGAGGAGTCACTTTGGGAGCTAGTTATTTGCCCTTTTCACTGTAAGGGGAAA 1945

1739 AGTTCCACAGGAGCGTGGCTCACCCAGCTCAACGTGGCTTCTCCCGGAGCAGTCCC 1798

1946 AGAAGGAATATGTTCAACATAAGATGATGGAGAAAGCAACGATGTATGGAATGTGATAT 2005

1799 ACAGGTCTACGTCCAGCACCTGTAAACAGACGAGAGCACCTGTGGAAGTTGATCG 1858

2006 CAGGGAGCGTTTATCTCTATGTGTGTGTGTCGCAAGGAAATGGCCAGAGATGTCATC 2065

1859 AAGGGGTGCCACATCTACGTCTGTGGGATGTCAGGAAACATGGCCAGGATGTGCAGA 1918

2066 GCAGTTGATACCATTTGCCAAGACAGGAGGACCATGGAATCATCTGTCTGCGGAGCTG 2125

1919 ACACCTTCTACGACATCGTGGCTGAGCTCGGGCCATGAGACGCGCAGGCGGTGAGCT 1978

2126 CAGTAAAGAACTCCAAAGTTGAAGAACGATATCTAAGAGATGTCTGGTGTATCGAATGTAG 2185

1979 ACATCAAGAACTGATGACCAAGGGCGCTACTCCCTGACGCTGTGGAGCTAGGGGCGCTG 2038

2186 CTTGCC 2191

2039 CTTGCC 2044

RESULT 4

US-09-313-294A-2366

; Sequence 2366, Application US/09313294A

; Patent No. 6476212

; GENERAL INFORMATION:

; APPLICANT: Ialugudi, Raghunath V.

; APPLICANT: Ito, Laura Y.

; APPLICANT: Sherman, Bradley K.

; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR

; FILE REFERENCE: PL-0017 US

; CURRENT APPLICATION NUMBER: US/09/313,294A

; CURRENT FILING DATE: 1999-05-14

; NUMBER OF SEQ ID NOS: 7600

; SOFTWARE: PERL Program

; SEQ ID NO 2366

; LENGTH: 260

; TYPE: DNA

; ORGANISM: Zea mays

; FEATURE:

NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700552557H1
US-09-313-294A-2366

Query Match 4.5%; Score 118.4; DB 4; Length 260;
Best Local Similarity 68.5%; Pred. No. 1.2e-25;
Matches 178; Conservative 0; Mismatches 81; Indels 1; Gaps 1;
QY 1890 CGTGAACGAGGAGTCAATTCGAGCTAGTTATTCCTTTTACGCTGAAGGGGAAAGAA 1949
Db 1 CCTGAGAGGGGCGCTTCTTGAGCTAATTTGTCATTTCTCGGGAAGGGCCACGAA 60
QY 1950 GGAATATGTTCAACATAGATGATGAGAAAGCAACGAGATGATGGAATGTGATATCAGG 2009
Db 61 AGAATATGTCAGCATAGATGTTGGAAGAGCCACAGATATTTGGAACATCATCTCAA 120
QY 2010 GGACGGTTATCTCTATGTTGTTGATGTCAGAGGGAATGCGCAGAGATGTCATCGCAC 2069
Db 121 TGGTGGTTACTTATATGTTTCCGCTGATGCCAAGGGAATGGCTAGAGATGTACACAAAT 180
QY 2070 GTTGTCATACCATGCCCAAGAACAGGACCCATGGAATCATCTGCTGCCGAAGCTGCAGT 2129
Db 181 GCT-CATCAATAGTCAGAGAGGATCTTTGGTAATCTCAAAACCGAGAGCTATGT 239
QY 2130 AAAGAACTCCAAAGTTGAAG 2149
Db 240 AAAGAGCTGCAGATGGAAG 259

RESULT 5

US-09-911-781-10
Sequence 10, Application US/09911781
Patent No. 6673613
GENERAL INFORMATION:
APPLICANT: Craft, David L.
APPLICANT: Wilson, C. Ron
APPLICANT: Birch, Dudley
APPLICANT: Zhang, Yeyan
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REFERENCE: U0012 OS/OAIP (1010-49)
CURRENT FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 3037
TYPE: DNA
ORGANISM: Candida tropicalis
US-09-911-781-10

Query Match 4.2%; Score 111.8; DB 4; Length 3037;
Best Local Similarity 54.3%; Pred. No. 7.4e-23;
Matches 271; Conservative 0; Mismatches 222; Indels 6; Gaps 2;
QY 1681 GTTCGAACGTCACAACTTCAAGTTACAGCTGACCCCTCAACTCCAATTATCATGTGGGA 1740
Db 2044 GTGAGAAGATCCAACTTTAAGTTGCCAAGAACTCCACACCCAGTATCTTGATGTT 2103
QY 1741 CTGGTACAGGGTTAGCTCTTTTACAGAGATTTCTGAGAAAGAAATGGCCCTCAAGGAA 1800
Db 2104 CCAGGTACTGGTGTGCCCCCATTTGAGAGGTTTCGTTAGAGAAAGAGTTCAACAAGTCAAG 2163
QY 1801 AATGGTGTCAACTTGGCCCGCAGTGTCTTTTTCGGATGTAGGAATCGTATATGAGC 1860
Db 2164 AATGGTGTCAATGTGGCAAGACTTTGTTGTTTATGTTGCGAAGAACTCCACGAGGAC 2223
QY 1861 TTCAATTTATGAAGCAAACTTAACAACTTCG---TGGAAACGAGGAGTCAATTCGGAGCTA 1917
Db 2224 TTTTGTGTAAGCAAGAAATGGCCCGCAGTACGCTTCTGTTTGGTGAAGAACTTCGAGATG 2283
QY 1918 GTTATGCTTTCACGTCGAGGGGAA---AAGAGGAATATGTTCAACATGAAGATG 1974
Db 2284 TTCAATGCTTCTCTAGCAAGACCCATCCAAAGAGGTTTACGTCAGGATGAATTTTA 2343
QY 1975 GAGAAAGCAACGGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTT 2034
Db 2344 GAAACAGCCAACTTGTGCACGAATTTGTGACGAGGTTGCCATTTATCTACGCTGTGTT 2403
QY 2035 GATGCCAAGGGAAATGGCCAGAGATGTCATCGCATCGCAGTGTGATACCATTCGCCCAAGAACAG 2094
Db 2284 TTTCAATGCTTCTCTAGCAAGACCCATCCAAAGAGGTTTACGTCAGGATGAATTTTA 2343

QY 1975 GAGAAAGCAACGGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTT 2034
Db 2344 GAAACAGCCAACTTGTGCACGAATTTGTGACGGAAGGTGCCATTTATCTACGCTGTGTT 2403
QY 2035 GATGCCAAGGGAAATGGCCAGAGATGTCATCGCAGTGTGATACCATTCGCCCAAGAACAG 2094
Db 2404 GACGCCAGTAGAATGGCCAGAGACGTCAGACCAAGATCTCCAGATTTGTTGCCAAAGC 2463
QY 2095 GACCCCATGGAATCATCTGCTGCCGAAGCTGCGAGTAAAGAACTCCAAAGTTGAAGAACGA 2154
Db 2464 AGAGAAATCAGTGAAGCAAGACGCGCTGAATTTGGTCAAGTCTCTGGAAGTCCAAAATAGA 2523
QY 2155 TATCTAAGAGATGCTCTGTT 2173
Db 2524 TACCAAGAAGATGTTTGGT 2542

RESULT 6

US-10-400-902-10
Sequence 10, Application US/10400902
Patent No. 6790640
GENERAL INFORMATION:
APPLICANT: Craft, David L.
APPLICANT: Wilson, C. Ron
APPLICANT: Birch, Dudley
APPLICANT: Zhang, Yeyan
TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
FILE REFERENCE: U0012 OS/OAIP (1010-49)
CURRENT FILING DATE: 2003-03-31
PRIOR FILING DATE: 2003-03-31
PRIOR FILING DATE: 2001-07-24
NUMBER OF SEQ ID NOS: 34
SOFTWARE: PatentIn version 3.1
SEQ ID NO 10
LENGTH: 3037
TYPE: DNA
ORGANISM: Candida tropicalis
US-10-400-902-10

Query Match 4.2%; Score 111.8; DB 4; Length 3037;
Best Local Similarity 54.3%; Pred. No. 7.4e-23;
Matches 271; Conservative 0; Mismatches 222; Indels 6; Gaps 2;
QY 1681 GTTCGAACGTCACAACTTCAAGTTACAGCTGACCCCTCAACTCCAATTATCATGTGGGA 1740
Db 2044 GTGAGAAGATCCAACTTTAAGTTGCCAAGAACTCCACACCCAGTATCTTGATGTT 2103
QY 1741 CTGGTACAGGGTTAGCTCTTTTACAGAGATTTCTGCGAAGAAAGATGCGCCCTCAAGGAA 1800
Db 2104 CCAGGTACTGGTGTGCCCCCATTTGAGAGGTTTCGTTAGAGAAAGAGTTCAACAAGTCAAG 2163
QY 1801 AATGGTGTCAACTTGGCCCGCAGTGTCTTTTTCGGATGTAGGAATCGTATATGAGC 1860
Db 2164 AATGGTGTCAATGTGGCAAGACTTTGTTGTTTATGTTGCGAAGAACTCCACGAGGAC 2223
QY 1861 TTCAATTTATGAAGCAAACTTAACAACTTCG---TGGAAACGAGGAGTCAATTCGGAGCTA 1917
Db 2224 TTTTGTGTAAGCAAGAAATGGCCCGCAGTACGCTTCTGTTTGGTGAAGAACTTCGAGATG 2283
QY 1918 GTTATGCTTTCACGTCGAGGGGAA---AAGAGGAATATGTTCAACATGAAGATG 1974
Db 2284 TTCAATGCTTCTCTAGCAAGACCCATCCAAAGAGGTTTACGTCAGGATGAATTTTA 2343
QY 1975 GAGAAAGCAACGGATGTATGGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTT 2034
Db 2344 GAAACAGCCAACTTGTGCACGAATTTGTGACGAGGTTGCCATTTATCTACGCTGTGTT 2403
QY 2035 GATGCCAAGGGAAATGGCCAGAGATGTCATCGCATCGCAGTGTGATACCATTCGCCCAAGAACAG 2094
Db 2404 GACGCCAGTAGAATGGCCAGAGACGTCAGACCAAGATCTCCAAAGATTTGTTGCCAAAGC 2463

GENERAL INFORMATION:
 ; APPLICANT: Craft, David L.
 ; APPLICANT: Wilson, C. Ron
 ; APPLICANT: Eirich, Dudley
 ; APPLICANT: Zhang, Yeyan
 ; TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
 ; FILE REFERENCE: U0012 OS/OA/P (1010-49)
 ; CURRENT APPLICATION NUMBER: US/09/911,781
 ; CURRENT FILING DATE: 2001-07-24
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 4145
 ; TYPE: DNA
 ; ORGANISM: Candida tropicalis
 US-09-911-781-3

Query Match 4.2%; Score 111.8; DB 4; Length 4145;
 Best Local Similarity 54.3%; Pred. No. 9.2e-23;
 Matches 271; Conservative 0; Mismatches 222; Indels 6; Gaps 2;

Qy	1681	GTTCGACGTCACAACTTCAAGTTTACAGCTGACCCCTCAACTCAATTCATATCATGGTGGGA	1740
Db	2572	GTGAGAAGATCCAACTTTAAGTTGCGCAAGAACTCCACACCCAGTTATCTTGTATGGT	2631
Qy	1741	CCTGGTACAGGGTTAGCTCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGAA	1800
Db	2632	CCAGGTACTGGTGTGCGCCCAATGAGAGGTTTCGTTAGAGAAAGAGTTCAACAAGTCAAG	2691
Qy	1801	AATGGTGCTCAACTTGGCCCGACAGTCTCTTTTCGGATGTAGGAATCGTAATATGGAC	1860
Db	2692	AATGGTGCTCAACTTGGCCCGACAGTCTCTTTTCGGATGTAGGAATCGTAATATGGAC	2751
Qy	1861	TTCAATTTATGAAGCAAGCACTTAACTTCG---TGGACGAGGAGTCAATTCGGAGCTA	1917
Db	2752	TTTTTGTACAAGCAAGAAATGGCGGAGTACGCTTCTGTTTGGTGAAAACCTTTGAGATG	2811
Qy	1918	GTTATTTGCTCTTTCAGCTGAAAGGGAA---AAGAAGGAATATGTTCAACATAGATGATG	1974
Db	2812	TTCAATGCTCTTCTAGACAGACCCATCCAAAGAGGTTTACGTCAGGATAGATTTTA	2871
Qy	1975	GAGAAGCAACGGATGTATGGAATGTATATCAGGGGACGTTATCTCTATGTGTGTGT	2034
Db	2872	GAACCAAGCCAACTTGTGACGAAATTTGTTGGTGAAAACCTTTGAGATG	2931
Qy	2035	GATGCCAAGGGAATGGCCAGAGATGTCATCGCACGTTGCATACCATTCGCCAAGAACAG	2094
Db	2932	GACGCCAGTAGAATGGCCAGAGACGTTCCAGACCCAGATCTCCAGATGTTGCCAAGC	2991
Qy	2095	GGACCCATGGAATCATCTGCTGCCGAAGCTGCAGTAAAGAACTCCAAAGTTGAAGAACGA	2154
Db	2992	AGAGAAATCAGTGAAGCAAGCAAGGCGCTGAAATGGTCAAGTCTCGAAGAGTCCAAAATAGA	3051
Qy	2155	TATCTAAGAGATGCTGTGT 2173	
Db	3052	TACCAAGAAGATGTTTGGT 3070	

RESULT 11
 US-09-302-620B-81
 ; Sequence 81, Application US/09302620B
 ; Patent No. 6331420
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilson, C. Ron
 ; APPLICANT: Craft, David L.
 ; APPLICANT: Eirich, Dudley
 ; APPLICANT: Eshoo, Mark
 ; APPLICANT: Madduri, Krishna M.
 ; APPLICANT: Cornett, Cathy A.
 ; APPLICANT: Brenner, Alfred A.
 ; APPLICANT: Tang, Maria
 ; APPLICANT: Loper, John C.
 ; APPLICANT: Gleeson, Martin
 ; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
 ; TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
 ; TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
 ; TITLE OF INVENTION: RELATING THERETO
 ; FILE REFERENCE: 1010-16 seq
 ; CURRENT APPLICATION NUMBER: US/09/302,620B
 ; CURRENT FILING DATE: 1999-04-30
 ; NUMBER OF SEQ ID NOS: 109
 ; SOFTWARE: PatentIn Ver. 2.1

GENERAL INFORMATION:
 ; APPLICANT: Craft, David L.
 ; APPLICANT: Wilson, C. Ron
 ; APPLICANT: Eirich, Dudley
 ; APPLICANT: Zhang, Yeyan
 ; TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
 ; FILE REFERENCE: U0012 OS/OA/P (1010-49)
 ; CURRENT APPLICATION NUMBER: US/09/911,781
 ; CURRENT FILING DATE: 2001-07-24
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 4145
 ; TYPE: DNA
 ; ORGANISM: Candida tropicalis
 US-10-400-902-3

Query Match 4.2%; Score 111.8; DB 4; Length 4145;
 Best Local Similarity 54.3%; Pred. No. 9.2e-23;
 Matches 271; Conservative 0; Mismatches 222; Indels 6; Gaps 2;

Qy	1681	GTTCGACGTCACAACTTCAAGTTTACAGCTGACCCCTCAACTCAATTCATATCATGGTGGGA	1740
Db	2572	GTGAGAAGATCCAACTTTAAGTTGCGCAAGAACTCCACACCCAGTTATCTTGTATGGT	2631
Qy	1741	CCTGGTACAGGGTTAGCTCTCTTTTCAGAGGATTTCTGCAGGAAAGAAATGGCCCTCAAGGAA	1800
Db	2632	CCAGGTACTGGTGTGCGCCCAATGAGAGGTTTCGTTAGAGAAAGAGTTCAACAAGTCAAG	2691
Qy	1801	AATGGTGCTCAACTTGGCCCGACAGTCTCTTTTCGGATGTAGGAATCGTAATATGGAC	1860
Db	2692	AATGGTGCTCAACTTGGCCCGACAGTCTCTTTTCGGATGTAGGAATCGTAATATGGAC	2751
Qy	1861	TTCAATTTATGAAGCAAGCACTTAACTTCG---TGGACGAGGAGTCAATTCGGAGCTA	1917
Db	2752	TTTTTGTACAAGCAAGAAATGGCGGAGTACGCTTCTGTTTGGTGAAAACCTTTGAGATG	2811
Qy	1918	GTTATTTGCTCTTTCAGCTGAAAGGGAA---AAGAAGGAATATGTTCAACATAGATGATG	1974
Db	2812	TTCAATGCTCTTCTAGACAGACCCATCCAAAGAGGTTTACGTCAGGATAGATTTTA	2871
Qy	1975	GAGAAGCAACGGATGTATGGAATGTATATCAGGGGACGTTATCTCTATGTGTGTGT	2034
Db	2872	GAACCAAGCCAACTTGTGACGAAATTTGTTGGTGAAAACCTTTGAGATG	2931
Qy	2035	GATGCCAAGGGAATGGCCAGAGATGTCATCGCACGTTGCATACCATTCGCCAAGAACAG	2094
Db	2932	GACGCCAGTAGAATGGCCAGAGACGTTCCAGACCCAGATCTCCAGATGTTGCCAAGC	2991
Qy	2095	GGACCCATGGAATCATCTGCTGCCGAAGCTGCAGTAAAGAACTCCAAAGTTGAAGAACGA	2154
Db	2992	AGAGAAATCAGTGAAGCAAGCAAGGCGCTGAAATGGTCAAGTCTCGAAGAGTCCAAAATAGA	3051
Qy	2155	TATCTAAGAGATGCTGTGT 2173	
Db	3052	TACCAAGAAGATGTTTGGT 3070	

RESULT 10
 US-10-400-902-3
 ; Sequence 3, Application US/10400902
 ; Patent No. 6790640
 ; GENERAL INFORMATION:
 ; APPLICANT: Craft, David L.
 ; APPLICANT: Wilson, C. Ron
 ; APPLICANT: Eirich, Dudley
 ; APPLICANT: Zhang, Yeyan
 ; TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
 ; FILE REFERENCE: U0012 OS/OA/P (1010-49)
 ; CURRENT APPLICATION NUMBER: US/10/400,902
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: US/09/911,781
 ; PRIOR FILING DATE: 2001-07-24

; SEQ ID NO 81		; LENGTH: 4206		; TYPE: DNA		; ORGANISM: Candida tropicalis		US-09-302-620B-81	
Query Match		4.1%; Score 108; DB 3; Length 4206;		Best Local Similarity 53.8%; Pred. No. 1.4e-21;		Matches 269; Conservative 0; Mismatches 225; Indels 6; Gaps 2;			
QY	1680	TGTTGCAAGCTCAAACTTCAAGTTACCACTGACCCCTCAACTCCCAATTAATCATGTGTGG	1739						
Db	2544	TGTGAGAAGATCCAACTTTAAAGTTGCCAAAGAACTCCACCCCAAGTTATCTTGATTGG	2603						
QY	1740	ACCTGGTACAGGTTAGCTCTTTTCAGAGGATTTTCGACGAGAAAGAAATGGCCCTCAAGGA	1799						
Db	2604	TCAGGTAAGATCCAACTTTAAAGTTGCCAAAGAACTCCACCCCAAGTTATCTTGATTGG	2663						
QY	1800	AAATGGTGTCAAGTTAGCTCTTTTCAGAGGATTTTCGACGAGAAAGAAATGGCCCTCAAGGA	1859						
Db	2664	GAATGGTGTCAAGTTAGCTCTTTTCAGAGGATTTTCGACGAGAAAGAAATGGCCCTCAAGGA	2723						
QY	1860	CTTCATTTATGAAGCAAGTAACTAACTTCG---TGGACGAGGAGTCAATTCGAGACT	1916						
Db	2724	CTTTTGTGTAAGCAAGTAACTAACTTCG---TGGACGAGGAGTCAATTCGAGACT	2783						
QY	1917	AGTTATTTGCTTTTTCAGGTGAAGGGGAA---AAGAGGAAATATGTTCAACATAAGATGAT	1973						
Db	2784	GTTCAATGCTTCTCCAGACAAGACCCATCCAAAGAGGTTTACGTCACGATAAGATTTT	2843						
QY	1974	GGAGAAAGCAACGGATGATATGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGG	2033						
Db	2844	AGAAAACAGCCAACTTGTGCAGAGTTGTGACTGAAGGTGCCATTTATCTACGCTGTGTGG	2903						
QY	2034	TGATGCCAAGGAAATGGCCAGAGATGTCATCGCAGGTTGCATACCAATTCGCCCAAGACA	2093						
Db	2904	TGATGCCAAGTGAATGGCTAGAGACGTGCAGACCAATTTCCAGATTTGTTGCTAAAG	2963						
QY	2094	GGGACCCATGGAATCATCTGCTGCCGAACTGCAGTAAAGAAACTCCAAAGTTGAAGAACG	2153						
Db	2964	CAGAGAAATAGTGAAGACAAGGCTGCTGAATTGGTCAAGTCTCTGGAAGTCCAAATAG	3023						
QY	2154	ATATCTAAGAGATGCTGGT 2173							
Db	3024	ATACCAAGAAGATGTTTGGT 3043							
RESULT 13									
US-09-911-781-2		; Sequence 2, Application US/09911781		; Patent No. 6673613		; GENERAL INFORMATION:			
		; APPLICANT: Craft, David L.		; APPLICANT: Wilson, C. Ron		; APPLICANT: Eirich, Dudley			
		; APPLICANT: Zhang, Yeyan		; FILE REFERENCE: U0012 OS/OAAP (1010-49)		; CURRENT APPLICATION NUMBER: US/09/911,781			
		; CURRENT FILING DATE: 2001-07-24		; NUMBER OF SEQ ID NOS: 34		; SOFTWARE: Patentin version 3.1			
		; SEQ ID NO 2		; LENGTH: 4206		; TYPE: DNA			
		; ORGANISM: Candida tropicalis		US-09-911-781-2					
Query Match		4.1%; Score 108; DB 4; Length 4206;		Best Local Similarity 53.8%; Pred. No. 1.4e-21;		Matches 269; Conservative 0; Mismatches 225; Indels 6; Gaps 2;			
QY	1680	TGTTGCAAGCTCAAACTTCAAGTTACCACTGACCCCTCAACTCCCAATTAATCATGTGTGG	1739						
Db	2544	TGTGAGAAGATCCAACTTTAAAGTTGCCAAAGAACTCCACCCCAAGTTATCTTGATTGG	2603						
QY	1740	ACCTGGTACAGGTTAGCTCTTTTCAGAGGATTTTCGACGAGAAAGAAATGGCCCTCAAGGA	1799						
Db	2604	TCAGGTAAGATCCAACTTTAAAGTTGCCAAAGAACTCCACCCCAAGTTATCTTGATTGG	2663						
QY	1800	AAATGGTGTCAAGTTAGCTCTTTTCAGAGGATTTTCGACGAGAAAGAAATGGCCCTCAAGGA	1859						
Db	2664	GAATGGTGTCAAGTTAGCTCTTTTCAGAGGATTTTCGACGAGAAAGAAATGGCCCTCAAGGA	2723						
QY	1860	CTTCATTTATGAAGCAAGTAACTAACTTCG---TGGACGAGGAGTCAATTCGAGACT	1916						
Db	2724	CTTTTGTGTAAGCAAGTAACTAACTTCG---TGGACGAGGAGTCAATTCGAGACT	2783						
QY	1917	AGTTATTTGCTTTTTCAGGTGAAGGGGAA---AAGAGGAAATATGTTCAACATAAGATGAT	1973						
Db	2784	GTTCAATGCTTCTCCAGACAAGACCCATCCAAAGAGGTTTACGTCACGATAAGATTTT	2843						
QY	1974	GGAGAAAGCAACGGATGATATGAATGTGATATCAGGGGACGGTTATCTCTATGTGTGTGG	2033						
Db	2844	AGAAAACAGCCAACTTGTGCAGAGTTGTGACTGAAGGTGCCATTTATCTACGCTGTGTGG	2903						
QY	2034	TGATGCCAAGGAAATGGCCAGAGATGTCATCGCAGGTTGCATACCAATTCGCCCAAGACA	2093						
Db	2904	TGATGCCAAGTGAATGGCTAGAGACGTGCAGACCAATTTCCAGATTTGTTGCTAAAG	2963						
QY	2094	GGGACCCATGGAATCATCTGCTGCCGAACTGCAGTAAAGAAACTCCAAAGTTGAAGAACG	2153						
Db	2964	CAGAGAAATAGTGAAGACAAGGCTGCTGAATTGGTCAAGTCTCTGGAAGTCCAAATAG	3023						
QY	2154	ATATCTAAGAGATGCTGGT 2173							
Db	3024	ATACCAAGAAGATGTTTGGT 3043							
RESULT 12									
US-09-912-161-3		; Sequence 3, Application US/09912161		; Patent No. 6503734		; GENERAL INFORMATION:			
		; APPLICANT: David, Krishna		; APPLICANT: Madduri, Krishna		; APPLICANT: Loper, John C.			
		; APPLICANT: Loper, John C.		; TITLE OF INVENTION: CYTOCHROME b5 GENE AND PROTEIN OF CANDIDA TROPICALIS AND METHODS		; TITLE OF INVENTION: THERETO			
		; FILE REFERENCE: M6368 (1010-35)		; CURRENT APPLICATION NUMBER: US/09/912,161		; CURRENT FILING DATE: 2001-07-24			
		; NUMBER OF SEQ ID NOS: 45		; SOFTWARE: Patentin version 3.1		; SEQ ID NO 3			
		; LENGTH: 4206		; TYPE: DNA		; ORGANISM: Candida tropicalis			
		US-09-912-161-3							
Query Match		4.1%; Score 108; DB 4; Length 4206;		Best Local Similarity 53.8%; Pred. No. 1.4e-21;		Matches 269; Conservative 0; Mismatches 225; Indels 6; Gaps 2;			
QY	1680	TGTTGCAAGCTCAAACTTCAAGTTACCACTGACCCCTCAACTCCCAATTAATCATGTGTGG	1739						

Qy 1860 CTTCAATTATGAAGACGAACTAAACAACTTCG---TGGAAACGAGAGTCAATTCGAGCT 1916
 Db 2724 CTTTTCGTACAGCAAGATGGCCGAGTACGCTTCGTTTGGTGAAACTTTGAGAT 2783
 Qy 1917 AGTTATTCGCTTTTCAGCTGAAGGGAA---AGAAGGAATATGTTCAAATAAGATGAT 1973
 Db 2784 GTTCAATGCTTCTCCAGACAAGACCCATCCAAAGAGTTTACGTCACAGATAAGATTTT 2843
 Qy 1974 GGAGAAACCAACGATGATGATATGATATCAGGGGACGGTTATCTCTATGCTGTGG 2033
 Db 2844 AGAAACAGCAACTTGTGCACAGTTGTTGACATGAAGGTGCCATATCTACGCTGTGG 2903
 Qy 2034 TGATGCCAAGGGAATGCCAGAGATGTCATCGCACGTTGCATACCAATTCGCCCAAGAACA 2093
 Db 2904 TGATGCCAGTAGAATGCTAGAGACGTGCAGACCAATTTCCAAGATTGTTGCTAAAG 2963
 Qy 2094 GGGACCCATGGAATCTCTGCTGCCGAAGCTGCGANGTAAGAAACTCCAAAGTTGAAGACG 2153
 Db 2964 CAGAGAAATTAGTGAAGACAAGGCTGCTGAATTGGTCAAGTCTCGAAGGTCCAAAATAG 3023
 Qy 2154 ATATCTAAGAGATCTCTGGT 2173
 Db 3024 ATACCAAGAAGATGTTTGGT 3043

RESULT 14
 US-10-400-902-2
 ; Sequence 2, Application US/10400902
 ; Patent No. 6790640
 ; GENERAL INFORMATION:
 ; APPLICANT: Craft, David L.
 ; APPLICANT: Wilson, C. Ron
 ; APPLICANT: Birch, Dudley
 ; APPLICANT: Zhang, Yeyan
 ; TITLE OF INVENTION: USE OF CYP52A2A PROMOTER TO INCREASE GENE EXPRESSION IN YEAST
 ; FILE REFERENCE: U0012 OS/ORAP (1010-49)
 ; CURRENT APPLICATION NUMBER: US/10/400,902
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: US/09/911,781
 ; PRIOR FILING DATE: 2001-07-24
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 4206
 ; TYPE: DNA
 ; ORGANISM: Candida tropicalis
 US-10-400-902-2

Query Match 4.1%; Score 108; DB 4; Length 4206;
 Best Local Similarity 53.8%; Pred. No. 1.4e-21;
 Matches 269; Conservative 0; Mismatches 225; Indels 6; Gaps 2;
 Qy 1680 TGTTCGACGTCAAACCTTCAAGTTACAGCTGACCCCTCAACTCCAAATTATCATGTGGG 1739
 Db 2544 TGTGAGAAGATCCAACTTTAAGTTGCCAAAGAACTCCACCACCCAGTTATCTTGATGG 2603
 Qy 1740 ACCTGGTACAGGGTAGCTCTTTCAGAGGATTTCTGCAGGAAGAAATGCCCTCAAGGA 1799
 Db 2604 TCCAGGTACTGGTGTGGCCCATGTGAGAGGTTTGTGCAGAGAAGAGTTCAACAAGTCAA 2663
 Qy 1800 AAATGGTGTCAACTTGGCCCGCAGAGTCTCTTTTTCGAGATGTAGGAATCGTAATATGGA 1859
 Db 2664 GAATGGTGTCAATGTTGGCAAGACTTGTGTTTATGTTGTTGAGAACTCCAAAGGGA 2723
 Qy 1860 CTTCAATTATGAAGACGAACTAAACAACTTCG---TGGAAACGAGAGTCAATTCGAGCT 1916
 Db 2724 CTTTTCGTACAGCAAGATGGGCCGAGTACGCTTCTGTTTGGTGAAACTTTGAGAT 2783
 Qy 1917 AGTTATTCGCTTTTCAGCTGAAGGGAA---AGAAGGAATATGTTCAAATAAGATGAT 1973
 Db 2784 GTTCAATGCTTCTCCAGACAAGACCCATCCAAAGAGTTTACGTCACAGATAAGATTTT 2843
 Qy 1974 GGAGAAACCAACGATGATGGAATGTGATATCAGGGGACGGTTATCTCTATGTTGGG 2033

Db 2844 AGAARACGCCAATTTGTGCAGAGTTGTTGACTGAAGGTGCCATATCTACGCTGTGG 2903
 Qy 2034 TGATGCCAAGGGAATGCCAGAGATGTCATCGCACGTTGCATACCAATTCGCCCAAGAACA 2093
 Db 2904 TGATGCCAGTAGAATGGCTAGAGACGTGCAGACCAATTTCCAAGATTGTTGCTAAAG 2963
 Qy 2094 GGGACCCATGGAATCATCTGCTGCCGAAGCTGCGANGTAAGAAACTCCAAAGTTGAAGACG 2153
 Db 2964 CAGAGAAATTAGTGAAGACAAGGCTGCTGAATTGGTCAAGTCTCGAAGGTCCAAAATAG 3023
 Qy 2154 ATATCTAAGAGATGTTTGGT 2173
 Db 3024 ATACCAAGAAGATGTTTGGT 3043

RESULT 15
 US-09-313-294A-2975
 ; Sequence 2975, Application US/09313294A
 ; Patent No. 6476212
 ; GENERAL INFORMATION:
 ; APPLICANT: Ialugudi, Raghunath V.
 ; APPLICANT: Ito, Laura Y.
 ; APPLICANT: Sherman, Bradley K.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
 ; FILE REFERENCE: PL-0017 US
 ; CURRENT APPLICATION NUMBER: US/09/313,294A
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 7600
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 2975
 ; LENGTH: 212
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6476212 700282102H1
 ; NAME/KEY: unsure
 ; LOCATION: 3' 9' 136
 ; OTHER INFORMATION: a, t, c, g, or other
 US-09-313-294A-2975

Query Match 3.9%; Score 103.8; DB 4; Length 212;
 Best Local Similarity 70.4%; Pred. No. 3.1e-21;
 Matches 138; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 Qy 952 GCTAACGGCGATGTTGCAATTTGATATTCCTTCATCTTCCTTGAGAACCAATTTGTTGCTCAACAA 1011
 Db 11 GCCAACGGTACTGTTGTTGATGATATTCACACCCCTTGACAGGTCTAATGTTGCTGCG 70
 Qy 1012 AGAGAGCTCCACAAACCCCAAGTCTGATAGATCTGTATACATCTGAGTTCGACATATCA 1071
 Db 71 AAGGAGCTGCACAAACCAAGCTTCAGATCGCTCTTGTATCATCTCGAGTTTGACATTTCT 130
 Qy 1072 GGCTCTTCCTTACATATGAGACTGGAGATCATGTTGGTGTGTTTATGCTCGAGAACTCGAT 1131
 Db 131 GGCACNGGTCTTGTGTATGAACCCGAGACCATGTTGGTGTATATCGAGAAATTCGTT 190
 Qy 1132 GAACTGTGAGGAAG 1147
 Db 191 CAGACTGTGAGGAGG 206

Search completed: October 19, 2005, 14:55:11
 Job time : 463 secs

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